OM protein - protein search, using sw model
Run on: October 31, 2006, 02:26:34 ; Search time 199 Seconds
(without alignments)
537.631 Million cell updates/sec

Title: US-10-063-518-14
Perfect score: 1195
Sequence: 1 MNHLPEDMENALTGSQSSHA...........EAGSEEAEEKQDSEKPLLEL 234
Scoring table: BLOSUM62
                      Gapop 10.0 , Gapext 0.5
Searched: 2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
Database :   Listing first 1500 summaries
                 A_Geneseq 8.*

                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003aas:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                    SUMMARIES

No.   Score Match Length DB ID   Description

RESULT 1
ID AAU29056 standard; protein; 234 AA.
DE Human PRO polypeptide sequence #33.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 2
ID AAM39929 standard; protein; 234 AA.
DE Human polypeptide SEQ ID NO 3074.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1195; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 3
ID AAB87532 standard; protein; 234 AA.
DE Human PRO1864.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 4
ID ABG95857 standard; protein; 234 AA.
DE Human secreted/transmembrane protein PRO1864.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 5; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 5
ID ABB84847 standard; protein; 234 AA.
DE Human PRO1864 protein sequence SEQ ID NO:62.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 5; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 6
ID ABB95453 standard; protein; 234 AA.
DE Human angiogenesis related protein PRO1864 SEQ ID NO: 62.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILL.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PAN J) PAN J.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1195; DB 5; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 7
ID ABU58432 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003022272-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 8
ID ABU87980 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 9
ID ABU84295 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 10
ID ABR66169 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 11
ID ABR65559 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 12
ID ABU82738 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 13
ID ABU99499 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 14
ID ABU89859 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036147-A1.

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PD   20-FEB-2003.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
ID   ABR68108 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027264-A1.
PD   06-FEB-2003.
RESULT 15
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
ID   ABU96161 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003036144-A1.
PD   20-FEB-2003.
RESULT 16
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
ID   ABU92592 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003035149-A1.
PD   20-FEB-2003.
RESULT 17
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
ID   ABU08669 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003044923-A1.
PD   06-MAR-2003.
RESULT 18
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
ID   AB002721 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003040062-A1.
PD   27-FEB-2003.
RESULT 19
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
ID   ABR74875 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040056-A1.
PD   27-FEB-2003.
RESULT 20
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
ID   ABR94637 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044926-A1.
PD   06-MAR-2003.
RESULT 21
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
ID   ABU85610 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003036140-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
RESULT 22
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
ID   ABU98770 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003013153-A1.
PD   16-JAN-2003.
RESULT 23
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
ID   ABU79985 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003017544-A1.
PD   23-JAN-2003.
RESULT 24
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
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     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
RESULT 25
ID   ABU91691 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003027277-A1.
PD   06-FEB-2003.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
RESULT 26
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
ID   ABU89384 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003036141-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
RESULT 27
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
ID   ABU62225 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036146-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
RESULT 28
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
ID   ABU67438 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036162-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
RESULT 29
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
ID   ABU80466 standard; protein; 234 AA.
DE   Human PRO protein #33.
PN   US2003036137-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
RESULT 30
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
ID   ABU90882 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003018173-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
RESULT 31
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
ID   ABO33941 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein PRO1864.
PN   US2003009013-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
RESULT 32
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
ID   ABR99384 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040063-A1.
PD   27-FEB-2003.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
RESULT 33
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
ID   ABR98774 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040064-A1.
PD   27-FEB-2003.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
RESULT 34
     Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
ID   ABO16297 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein
PN   US2003027267-A1.
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PD· 06-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 35
ID ABR92197 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030360160-A1.
PD 20-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 36
ID ABO18838 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030544925-A1.
PD 06-MAR-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 37
ID ABR78259 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030054474-A1.
PD 20-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 38
ID ABR39937 standard; protein; 234 AA.
DE Human prostate selective polypeptide Pr340.
PN WO200014298-A2.
PD 20-FEB-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 39
ID ABU71958 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20030018183-A1.
PD 23-JAN-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 40
ID ABU84995 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20030032114-A1.
PD 13-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 41
ID ABO00134 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20030032101-A1.
PD 13-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 42
ID ABO11466 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030036124-A1.
PD 20-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 43
ID ABO02111 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030044054-A1.
PD 27-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 44
ID ABU88685 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20030036133-A1.
PD 20-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 45
ID ABU83380 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030036134-A1.
PD 20-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 46
ID ABO06181 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20030222294-A1.
PD 30-JAN-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 47
ID ABR59217 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030277275-A1.
PD 06-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 48
ID ABO09279 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030327324-A1.
PD 06-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 49
ID ABO19143 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20030361118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 50
ID ABO11161 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030036123-A1.
PD 20-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 51
ID ABR66779 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030036148-A1.
PD 20-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 52
ID ABO15992 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030040060-A1.
PD 27-FEB-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 53
ID ABO13698 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030044916-A1.
PD 06-MAR-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 54
ID ABU71512 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864.
PN US20030013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 55
ID   ABU65601 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein, SEQ ID 66.
PN   US20030036156-A1.
PD   20-FEB-2003.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 56
ID   ABO07449 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030032117-A1.
PD   13-FEB-2003.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 57
ID   ABO03636 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030027266-A1.
PD   06-FEB-2003.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 58
ID   ABR67084 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO.66.
PN   US20030054483-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 59
ID   ABO15687 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein, PRO1864.
PN   US20030022298-A1.
PD   30-JAN-2003.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 60
ID   ABU55968 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US20020182638-A1.
PD   05-DEC-2002.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 61
ID   ABU72293 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US20030032117-A1.
PD   13-FEB-2003.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 62
ID   ABU55296 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030036117-A1.
PD   20-FEB-2003.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 63
ID   ABU95241 standard; protein; 234 AA.
DE   Human PRO1864 protein.
PN   US20030032102-A1.
PD   13-FEB-2003.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 64
ID   ABU71144 standard; protein; 234 AA.
DE   Human PRO1864 protein.
PN   US20030036143-A1.
PD   06-FEB-2003.

Query Match

Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 65
ID   ABO07754 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030032130-A1.
PD   13-FEB-2003.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 66
ID   ABR69995 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO.66.
PN   US20030032118-A1.
PD   20-FEB-2003.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 67
ID   ABR69328 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO.66.
PN   US20030036132-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 68
ID   ABO01469 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030008353-A1.
PD   09-JAN-2003.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 69
ID   ABU81271 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030017542-A1.
PD   23-JAN-2003.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 70
ID   ABR60068 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO.66.
PN   US20030032137-A1.
PD   13-FEB-2003.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 71
ID   ABR58287 standard; protein; 234 AA.
DE   BCU0092 protein #SEQ ID 20.
PN   WO200302921-A2.
PD   10-APR-2003.
PA   (ORIG-) ORIGENE TECHNOLOGIES INC.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 72
ID   ABU90966 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO.66.
PN   US20030018168-A1.
PD   23-JAN-2003.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 73
ID   ABR67803 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO.66.
PN   US20030027269-A1.
PD   06-FEB-2003.

Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 74
ID   ABR65191 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO.66.
PN   US20030027268-A1.
PD   06-FEB-2003.

Query Match

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Query Match            100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 75
ID   ABR68413 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027274-A1.
PD   06-FEB-2003.

RESULT 76
ID   ABR71825 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003032135-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.

Query Match            100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 77
ID   ABU85305 standard; protein; 234 AA.
DE   Human PRO polypeptide protein #33.
PN   US2003022295-A1.
PD   30-JAN-2003.

Query Match            100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 78
ID   ABU88995 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003022297-A1.
PD   30-JAN-2003.

Query Match            100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 79
ID   ABU83075 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003032105-A1.
PD   13-FEB-2003.

Query Match            100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 80
ID   ABU94931 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003032123-A1.
PD   13-FEB-2003.

Query Match            100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 81
ID   ABU90479 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003032108-A1.
PD   13-FEB-2003.

Query Match            100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 82
ID   ABU83990 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003032111-A1.
PD   13-FEB-2003.

Query Match            100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 83
ID   ABU93641 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003032119-A1.
PD   13-FEB-2003.

Query Match            100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 84
ID   ABR64886 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027263-A1.
PD   06-FEB-2003.

Query Match            100.0%;  Score 1195;  DB 6;  Length 234;


Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 85
ID   ABO27287 standard; protein; 234 AA.
DE   Human secreted/transmembrane polypeptide PRO1864.
PN   US2003009012-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.

RESULT 86
ID   ABR68718 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027271-A1.
PD   06-FEB-2003.

Query Match            100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 87
ID   ABO06534 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036125-A1.
PD   20-FEB-2003.

Query Match            100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 88
ID   ABR99079 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040068-A1.
PD   27-FEB-2003.

Query Match            100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 89
ID   ABU56963 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003027280-A1.
PD   06-FEB-2003.

Query Match            100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 90
ID   ABU85915 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003022300-A1.
PD   30-JAN-2003.

Query Match            100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 91
ID   ABU82202 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003036136-A1.
PD   20-FEB-2003.

Query Match            100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 92
ID   ABU87213 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003036138-A1.
PD   20-FEB-2003.

Query Match            100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 93
ID   ABU83685 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003032109-A1.
PD   13-FEB-2003.

Query Match            100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 94
ID   ABO08059 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003040066-A1.
PD   27-FEB-2003.

Query Match            100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity  100.0%;  Pred. No. 1.6e-131;

RESULT 95
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ID ABU92482 standard; protein; 234 AA.
DE Human secreted/transmembrane protein PRO1864.
PN US20030045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.

RESULT 96
ID ABU81770 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20030032104-A1.
PN US20030036157-A1.
PD 13-FEB-2003.
PD 20-FEB-2003.

Query Match   100.0%;   Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 97
ID ABU65934 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20030027212-A1.
PD 06-FEB-2003.

Query Match   100.0%;   Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 98
ID ABU81152 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20030032120-A1.
PD 13-FEB-2003.

Query Match   100.0%;   Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 99
ID ABR59763 standard; protein; 234 AA.
DE Human secreted and transmembrane polypeptide PRO1864, SEQ ID NO:66.
PN US20030036155-A1.
PD 20-FEB-2003.

Query Match   100.0%;   Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 100
ID ABU93951 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20030032296-A1.
PD 30-JAN-2003.

Query Match   100.0%;   Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 101
ID ABU99804 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20030027281-A1.
PD 06-FEB-2003.

Query Match   100.0%;   Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 102
ID ABR66474 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030022301-A1.
PD 30-JAN-2003.

Query Match   100.0%;   Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 103
ID ABR90892 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030027986-A1.
PD 27-FEB-2003.

Query Match   100.0%;   Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 104
ID ABO53267 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20030027986-A1.
PD 06-FEB-2003.

Query Match   100.0%;   Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 105
ID ABU94319 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US20030017540-A1.
PD 23-JAN-2003.

Query Match   100.0%;   Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 106
ID ABU79201 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US20030032106-A1.
PD 13-FEB-2003.

Query Match   100.0%;   Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 107
ID ABU86530 standard; protein; 234 AA.
DE Novel human secreted/transmembrane protein (PRO) #33.
PN US20030032129-A1.
PD 13-FEB-2003.

Query Match   100.0%;   Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 108
ID ABU86835 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US20030032103-A1.
PD 13-FEB-2003.

Query Match   100.0%;   Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 109
ID ABU94624 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US20030032131-A1.
PD 13-FEB-2003.

Query Match   100.0%;   Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 110
ID ABO04551 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US20030032107-A1.
PD 13-FEB-2003.

Query Match   100.0%;   Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 111
ID ABR70300 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030032139-A1.
PD 13-FEB-2003.

Query Match   100.0%;   Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 112
ID ABU98465 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US20030022301-A1.
PD 30-JAN-2003.

Query Match   100.0%;   Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 113
ID ABR65864 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030036165-A1.
PD 20-FEB-2003.

Query Match   100.0%;   Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 114
ID ABR64581 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030027262-A1.
PD 06-FEB-2003.

Query Match   100.0%;   Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 115
ID ABU79506 standard; protein; 234 AA.

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DE   Human PRO polypeptide #33.
PN   US2003032110-A1.
PD   13-FEB-2003.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                             100.0%;   Pred. No. 1.6e-131;

RESULT 116
ID   ABU92897 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036142-A1.
PD   20-FEB-2003.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                             100.0%;   Pred. No. 1.6e-131;

RESULT 117
ID   ABU95856 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003036145-A1.
PD   20-FEB-2003.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                             100.0%;   Pred. No. 1.6e-131;

RESULT 118
ID   ABU91076 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003036154-A1.
PD   20-FEB-2003.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                             100.0%;   Pred. No. 1.6e-131;

RESULT 119
ID   ABU90169 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003036153-A1.
PD   20-FEB-2003.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                             100.0%;   Pred. No. 1.6e-131;

RESULT 120
ID   ABO09584 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003044931-A1.
PD   06-MAR-2003.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                             100.0%;   Pred. No. 1.6e-131;

RESULT 121
ID   ABO10856 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003040069-A1.
PD   27-FEB-2003.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                             100.0%;   Pred. No. 1.6e-131;

RESULT 122
ID   ABR70910 standard; protein; 234 AA.
DE   Novel human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2002183493-A1.
PD   05-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                             100.0%;   Pred. No. 1.6e-131;

RESULT 123
ID   ABU98269 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003022293-A1.
PD   30-JAN-2003.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                             100.0%;   Pred. No. 1.6e-131;

RESULT 124
ID   ABU87518 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003027993-A1.
PD   06-FEB-2003.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                             100.0%;   Pred. No. 1.6e-131;

RESULT 125
ID   ABU91386 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein #33.
PN   US2003032128-A1.
PD   13-FEB-2003.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                             100.0%;   Pred. No. 1.6e-131;

RESULT 126
ID   ABU89274 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003036634-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                             100.0%;   Pred. No. 1.6e-131;

RESULT 127
ID   ABU84600 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003032116-A1.
PD   13-FEB-2003.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                             100.0%;   Pred. No. 1.6e-131;

RESULT 128
ID   ABR69690 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003032122-A1.
PD   13-FEB-2003.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                             100.0%;   Pred. No. 1.6e-131;

RESULT 129
ID   ABU80067 standard; protein; 234 AA.
DE   Human PRO protein #33.
PN   US2003036139-A1.
PD   20-FEB-2003.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                             100.0%;   Pred. No. 1.6e-131;

RESULT 130
ID   ABU82481 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2002183494-A1.
PD   05-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                             100.0%;   Pred. No. 1.6e-131;

RESULT 131
ID   ABU93336 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003017541-A1.
PD   23-JAN-2003.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                             100.0%;   Pred. No. 1.6e-131;

RESULT 132
ID   ABO09889 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003017543-A1.
PD   23-JAN-2003.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                             100.0%;   Pred. No. 1.6e-131;

RESULT 133
ID   ABO08974 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036152-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                             100.0%;   Pred. No. 1.6e-131;

RESULT 134
ID   ABU96445 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003027993-A1.
PD   06-FEB-2003.
     Query Match
     Best Local Similarity   100.0%;   Score 1195;   DB 6;   Length 234;
                             100.0%;   Pred. No. 1.6e-131;

RESULT 135
ID   ABU10542 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein #33.
PN   US2002127584-A1.
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PD   12-SEP-2002.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;  Score 1195;   DB 6;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;   Length 234;

RESULT 136
ID   ABU72115 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US20030232042-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;  Score 1195;   DB 6;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;   Length 234;

RESULT 137
ID   ABU95551 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030232115-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;  Score 1195;   DB 6;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;   Length 234;

RESULT 138
ID   ABU95760 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030232140-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;  Score 1195;   DB 6;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;   Length 234;

RESULT 139
ID   ABR70605 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO.66.
PN   US20030040076-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;  Score 1195;   DB 6;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;   Length 234;

RESULT 140
ID   ABO04956 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030008352-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;  Score 1195;   DB 6;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;   Length 234;

RESULT 141
ID   ABO08364 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030044922-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;  Score 1195;   DB 6;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;   Length 234;

RESULT 142
ID   ABO05571 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030032118-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;  Score 1195;   DB 6;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;   Length 234;

RESULT 143
ID   ABR73960 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO.66.
PN   US20030036135-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;  Score 1195;   DB 6;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;   Length 234;

RESULT 144
ID   ABR95552 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO.66.
PN   US20030054455-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;  Score 1195;   DB 6;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;   Length 234;

RESULT 145
ID   ABR80849 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO.66.
PN   US20030049741-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;  Score 1195;   DB 6;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;   Length 234;

RESULT 146
ID   ABR81154 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO.66.
PN   US20030049743-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;  Score 1195;   DB 6;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;   Length 234;

RESULT 147
ID   ABM00850 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO.66.
PN   US20030049769-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;  Score 1195;   DB 6;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;   Length 234;

RESULT 148
ID   ABR88452 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO.66.
PN   US20030068743-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;  Score 1195;   DB 6;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;   Length 234;

RESULT 149
ID   ABM77273 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030054479-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;  Score 1195;   DB 6;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;   Length 234;

RESULT 150
ID   ABO28757 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068685-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;  Score 1195;   DB 6;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;   Length 234;

RESULT 151
ID   ABO31502 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068725-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;  Score 1195;   DB 6;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;   Length 234;

RESULT 152
ID   ABM07919 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO.66.
PN   US20030068752-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;  Score 1195;   DB 6;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;   Length 234;

RESULT 153
ID   ABO40399 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068682-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;  Score 1195;   DB 6;
Best Local Similarity 100.0%;  Pred. No. 1.6e-131;   Length 234;

RESULT 154
ID   ABO35824 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
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PN US20030687001-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

RESULT 155
Best Local Similarity 100.0%;
Query Match 100.0%; Score 1195; DB 6; Length 234;
ID ABO43963 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US20030068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

RESULT 156
Best Local Similarity 100.0%;
Query Match 100.0%; Score 1195; DB 6; Length 234;
ID ADA77818 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

RESULT 157
Best Local Similarity 100.0%;
Query Match 100.0%; Score 1195; DB 6; Length 234;
ID ABM24758 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

RESULT 158
Best Local Similarity 100.0%;
Query Match 100.0%; Score 1195; DB 6; Length 234;
ID ABO03026 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

RESULT 159
Best Local Similarity 100.0%;
Query Match 100.0%; Score 1195; DB 6; Length 234;
ID ABR90282 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

RESULT 160
Best Local Similarity 100.0%;
Query Match 100.0%; Score 1195; DB 6; Length 234;
ID ABM17196 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

RESULT 161
Best Local Similarity 100.0%;
Query Match 100.0%; Score 1195; DB 6; Length 234;
ID ABR94942 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.

RESULT 162
Best Local Similarity 100.0%;
Query Match 100.0%; Score 1195; DB 6; Length 234;
ID ABR95247 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030044071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

RESULT 163
Best Local Similarity 100.0%;
Query Match 100.0%; Score 1195; DB 6; Length 234;
ID ADB17071 standard; protein; 234 AA.
DE Human transmembrane PRO polypeptide (SeqID 14).
PN US20030050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

RESULT 164
Best Local Similarity 100.0%;
Query Match 100.0%; Score 1195; DB 6; Length 234;
ID ABO21485 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

RESULT 165
Best Local Similarity 100.0%;
Query Match 100.0%; Score 1195; DB 6; Length 234;
ID ABR97749 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

RESULT 166
Best Local Similarity 100.0%;
Query Match 100.0%; Score 1195; DB 6; Length 234;
ID ABR87537 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

RESULT 167
Best Local Similarity 100.0%;
Query Match 100.0%; Score 1195; DB 6; Length 234;
ID ABM77578 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030054473-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

RESULT 168
Best Local Similarity 100.0%;
Query Match 100.0%; Score 1195; DB 6; Length 234;
ID ABM27808 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

RESULT 169
Best Local Similarity 100.0%;
Query Match 100.0%; Score 1195; DB 6; Length 234;
ID ABM06089 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

RESULT 170
Best Local Similarity 100.0%;
Query Match 100.0%; Score 1195; DB 6; Length 234;
ID ABM03595 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

RESULT 171
Best Local Similarity 100.0%;
Query Match 100.0%; Score 1195; DB 6; Length 234;
ID ABM35046 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

RESULT 172
Best Local Similarity 100.0%;
Query Match 100.0%; Score 1195; DB 6; Length 234;
ID ABM26283 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

RESULT 173
ID ABO48065 standard; protein; 234 AA.

DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030049749-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6;
     Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 174
ID   ABR92807 standard; protein; 234 AA.   Length 234;
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030064462-A1.
PN   US20030065159-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6;
     Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 175
ID   ABO24568 standard; protein; 234 AA.   Length 234;
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030064447-A1.
PN   US20030073184-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6;
     Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 176
ID   ABM11579 standard; protein; 234 AA.   Length 234;
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030065159-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6;
     Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 177
ID   ABM02680 standard; protein; 234 AA.   Length 234;
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030064451-A1.
PN   US20030064463-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6;
     Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 178
ID   ABO27537 standard; protein; 234 AA.   Length 234;
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030064451-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6;
     Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 179
ID   ABM29028 standard; protein; 234 AA.   Length 234;
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068721-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6;
     Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 180
ID   ABM07004 standard; protein; 234 AA.   Length 234;
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068699-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6;
     Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 181
ID   ABM07004 standard; protein; 234 AA.   Length 234;
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068699-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6;
     Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 182
ID   ABM21098 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.

PN   US20030068707-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6;
     Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 183
ID   ABM09444 standard; protein; 234 AA.   Length 234;
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030073175-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6;
     Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 184
ID   ABO41314 standard; protein; 234 AA.   Length 234;
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030066695-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6;
     Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 185
ID   ABO36129 standard; protein; 234 AA.   Length 234;
DE   Human PRO polypeptide #33.
PN   US20030068703-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6;
     Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 186
ID   ABO43658 standard; protein; 234 AA.   Length 234;
DE   Human PRO polypeptide #33.
PN   US20030068732-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6;
     Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 187
ID   ABM76358 standard; protein; 234 AA.   Length 234;
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030082717-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6;
     Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 188
ID   ABM76054 standard; protein; 234 AA.   Length 234;
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030104548-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6;
     Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 189
ID   ABM25673 standard; protein; 234 AA.   Length 234;
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030104542-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6;
     Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 190
ID   ABM25978 standard; protein; 234 AA.   Length 234;
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030104543-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6;
     Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 191
ID   ABO03331 standard; protein; 234 AA.   Length 234;
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030103127-A1.
PD   20-FEB-2003.
     Query Match   100.0%;
     Best Local Similarity 100.0%;

RESULT 192
ID   ABO02416 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003040061-A1.
PD   27-FEB-2003.

RESULT 193
ID   ABO44245 standard; protein; 234 AA.
DE   Human secreted/transmembrane polypeptide PRO 1864.
PN   US2003018172-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 194
ID   ABR90587 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036130-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 195
ID   ABR73655 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054468-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 196
ID   ABO16907 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003054470-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 197
ID   ABR94332 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044917-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 198
ID   ABR75839 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044929-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 199
ID   ABR71215 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003059880-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 200
ID   ABR93112 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064465-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 201
ID   ABR93417 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054478-A1.
PD   20-MAR-2003.

RESULT 202
ID   ABR87842 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068718-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 203
ID   ABO27842 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003064454-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 204
ID   ABO29977 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003064461-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 205
ID   ABO33186 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068724-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 206
ID   ABM04874 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068727-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 207
ID   ABM08834 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068772-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 208
ID   ABO36434 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068714-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 209
ID   ABO35519 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068758-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 6;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 210
ID   ABO39484 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068776-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.

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Query Match              100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;

RESULT 211
ID   ABM10359 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003069407-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;

RESULT 212
ID   ABM11884 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104555-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;

RESULT 213
ID   AB052030 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003049768-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;

RESULT 214
ID   AB052335 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003049771-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;

RESULT 215
ID   ADA19876 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003069394-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;

RESULT 216
ID   AB023653 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003032134-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;

RESULT 217
ID   ADB17259 standard; protein; 234 AA.
DE   Human transmembrane PRO polypeptide (SeqID 14).
PN   US2003050465-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;

RESULT 218
ID   ABR97139 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054481-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;

RESULT 219
ID   ABR86927 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049778-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;


RESULT 220
ID   ABM10969 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049782-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;

RESULT 221
ID   ABM28813 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054476-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;

RESULT 222
ID   AB032112 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068733-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;

RESULT 223
ID   ABM15239 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068692-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;

RESULT 224
ID   ABM06394 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068709-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;

RESULT 225
ID   ABM04205 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068716-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;

RESULT 226
ID   ABM22318 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068740-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;

RESULT 227
ID   ABM07614 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068751-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;

RESULT 228
ID   AB040704 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068684-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match              100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity    100.0%;  Pred. No. 1.6e-131;

RESULT 229
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ID   ABM35351 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073179-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 100.0%; Pred. No. 1.6e-131;
     Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

RESULT 230
ID   ABM33114 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003087374-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match 100.0%; Pred. No. 1.6e-131;
     Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

RESULT 231
ID   ABO52640 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003049773-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 100.0%; Pred. No. 1.6e-131;
     Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

RESULT 232
ID   ABO50200 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049777-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 100.0%; Pred. No. 1.6e-131;
     Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

RESULT 233
ID   ABU09194 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003040055-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match 100.0%; Pred. No. 1.6e-131;
     Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

RESULT 234
ID   ABO04246 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003035164-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match 100.0%; Pred. No. 1.6e-131;
     Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

RESULT 235
ID   ABO05876 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003040074-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match 100.0%; Pred. No. 1.6e-131;
     Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

RESULT 236
ID   ABM18416 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054480-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 100.0%; Pred. No. 1.6e-131;
     Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

RESULT 237
ID   ABR97444 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003059885-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 100.0%; Pred. No. 1.6e-131;
     Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

RESULT 238
ID   ABR80544 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049740-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 100.0%; Pred. No. 1.6e-131;
     Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

RESULT 239
ID   ABM01155 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049770-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 100.0%; Pred. No. 1.6e-131;
     Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

RESULT 240
ID   ABR88757 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073169-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 100.0%; Pred. No. 1.6e-131;
     Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

RESULT 241
ID   ABM13409 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064457-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 100.0%; Pred. No. 1.6e-131;
     Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

RESULT 242
ID   ABM20793 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068711-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 100.0%; Pred. No. 1.6e-131;
     Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

RESULT 243
ID   ABO41924 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049745-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 100.0%; Pred. No. 1.6e-131;
     Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

RESULT 244
ID   ABO42534 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049751-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 100.0%; Pred. No. 1.6e-131;
     Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

RESULT 245
ID   ABM10054 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003067478-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 100.0%; Pred. No. 1.6e-131;
     Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

RESULT 246
ID   ABO38569 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068773-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 100.0%; Pred. No. 1.6e-131;
     Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

RESULT 247
ID   ABM32809 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073185-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match 100.0%; Pred. No. 1.6e-131;
     Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;

RESULT 248
ID   ABM22623 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030087373-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 249
ID   ABM74834 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030096353-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 250
ID   ADA79610 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030073173-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 251
ID   ABR96224 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030054458-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 252
ID   ABM02375 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030059886-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 253
ID   ABR88317 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049758-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 254
ID   ABR86622 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049772-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 255
ID   ABM16586 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030064448-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 256
ID   ABM29638 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030064456-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 257
ID   ABO29062 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068693-A1.
PD   10-APR-2003.

RESULT 258
ID   ABM23843 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068735-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 259
ID   ABM23233 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068753-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 260
ID   ABM22013 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068742-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 261
ID   ABO37654 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068756-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 262
ID   ABM28418 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030082716-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 263
ID   ABM28723 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030082737-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 264
ID   ABM66367 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030104547-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 265
ID   ABM75749 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030096359-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 266
ID   ABM34029 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030101104-A1.
PD   10-APR-2003.
Query Match   100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity   100.0%;

RESULT 267
ID   ABM34334 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20031010061-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 268
ID   ABO20265 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030732125-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 269
ID   ABO21180 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030544454-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 270
ID   ABO22095 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030544777-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 271
ID   ADA20048 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20030060601-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 272
ID   ABO34173 standard; protein; 234 AA.
DE   Human secreted/transmembrane polypeptide PRO 1864.
PN   US20030054460-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 273
ID   ABR96529 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864.
PN   US20030049753-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 274
ID   ABR85707 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049763-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 275
ID   ABR99689 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030092121-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 276
ID   ABM00545 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.

RESULT 277
PN   US20030073172-A1.
PD   17-APR-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 277
ID   ABM00240 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030073172-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 278
ID   ABO29672 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068700-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 279
ID   ABM23538 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068736-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 280
ID   ABM29333 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068767-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 281
ID   ABO38264 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068679-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 282
ID   ABO45564 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030073182-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 283
ID   ABM20488 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030104557-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 284
ID   ADA81337 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030092121-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1195; DB 6; Length 234;
     Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 285
ID   ABO16602 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030027276-A1.
PD   06-FEB-2003.
     Query Match   100.0%; Score 1195; DB 6; Length 234;

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RESULT 286
ID   AB018228 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003044920-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 287
ID   AB022655 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003027265-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 288
ID   AB022960 standard; protein; 234 AA.
DE   Human PRO polypeptide; 234 AA.
PN   US2003054461-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 289
ID   ABR92502 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064446-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 290
ID   ABR81459 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049744-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 291
ID   ABM77883 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049783-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 292
ID   ABR89672 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073171-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 293
ID   ABM26588 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003032121-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 294
ID   ABM13714 standard; protein; 234 AA.
DE   Human secreted polypeptide; 234 AA.
PN   US2003064458-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 295
ID   ABO28452 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003064460-A1.
PN   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 296
ID   AB030282 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003064464-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 297
ID   ABM07309 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068702-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 298
ID   ABM03900 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068734-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 299
ID   AB037044 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068719-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 300
ID   AB041619 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003068729-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 301
ID   AB035214 standard; protein; 234 AA.
DE   Human PRO polypeptide; 234 AA.
PN   US2003068738-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 302
ID   ABM25063 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104540-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 303
ID   AB047455 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049742-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 304
ID   ABO47760 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049747-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;  Score 1195;  DB 6;  Length 234;
Best Local Similarity   100.0%;  Pred. No. 1.6e-131;
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RESULT 305
ID   ABO48370 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049750-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
  Query Match
  Best Local Similarity   100.0%;
  100.0%;   Score 1195;   DB 6;   Pred. No. 1.6e-131;   Length 234;

RESULT 306
ID   ABO51420 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003049766-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
  Query Match
  Best Local Similarity   100.0%;
  100.0%;   Score 1195;   DB 6;   Pred. No. 1.6e-131;   Length 234;

RESULT 307
ID   ABO51725 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003049767-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
  Query Match
  Best Local Similarity   100.0%;
  100.0%;   Score 1195;   DB 6;   Pred. No. 1.6e-131;   Length 234;

RESULT 308
ID   ABO50505 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049779-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
  Query Match
  Best Local Similarity   100.0%;
  100.0%;   Score 1195;   DB 6;   Pred. No. 1.6e-131;   Length 234;

RESULT 309
ID   ABR79629 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040059-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
  Query Match
  Best Local Similarity   100.0%;
  100.0%;   Score 1195;   DB 6;   Pred. No. 1.6e-131;   Length 234;

RESULT 310
ID   ABM16891 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040078-A1.
PD   27-FEB-2003
PA   (GETH) GENENTECH INC.
  Query Match
  Best Local Similarity   100.0%;
  100.0%;   Score 1195;   DB 6;   Pred. No. 1.6e-131;   Length 234;

RESULT 311
ID   ABO17923 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003044918-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
  Query Match
  Best Local Similarity   100.0%;
  100.0%;   Score 1195;   DB 6;   Pred. No. 1.6e-131;   Length 234;

RESULT 312
ID   ABO20875 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003032132-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
  Query Match
  Best Local Similarity   100.0%;
  100.0%;   Score 1195;   DB 6;   Pred. No. 1.6e-131;   Length 234;

RESULT 313
ID   ABR96834 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054462-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
  Query Match
  Best Local Similarity   100.0%;
  100.0%;   Score 1195;   DB 6;   Pred. No. 1.6e-131;   Length 234;

RESULT 314
ID   ABM12189 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064445-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
  Query Match
  Best Local Similarity   100.0%;
  100.0%;   Score 1195;   DB 6;   Pred. No. 1.6e-131;   Length 234;

RESULT 315
ID   ABM16281 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064449-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
  Query Match
  Best Local Similarity   100.0%;
  100.0%;   Score 1195;   DB 6;   Pred. No. 1.6e-131;   Length 234;

RESULT 316
ID   ABM24148 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064441-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
  Query Match
  Best Local Similarity   100.0%;
  100.0%;   Score 1195;   DB 6;   Pred. No. 1.6e-131;   Length 234;

RESULT 317
ID   ABM14629 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068696-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
  Query Match
  Best Local Similarity   100.0%;
  100.0%;   Score 1195;   DB 6;   Pred. No. 1.6e-131;   Length 234;

RESULT 318
ID   ABM04510 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068712-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
  Query Match
  Best Local Similarity   100.0%;
  100.0%;   Score 1195;   DB 6;   Pred. No. 1.6e-131;   Length 234;

RESULT 319
ID   ABM06699 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068730-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
  Query Match
  Best Local Similarity   100.0%;
  100.0%;   Score 1195;   DB 6;   Pred. No. 1.6e-131;   Length 234;

RESULT 320
ID   ABM09139 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068775-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
  Query Match
  Best Local Similarity   100.0%;
  100.0%;   Score 1195;   DB 6;   Pred. No. 1.6e-131;   Length 234;

RESULT 321
ID   ABO39179 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003073174-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
  Query Match
  Best Local Similarity   100.0%;
  100.0%;   Score 1195;   DB 6;   Pred. No. 1.6e-131;   Length 234;

RESULT 322
ID   ABM75444 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104545-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
  Query Match
  Best Local Similarity   100.0%;
  100.0%;   Score 1195;   DB 6;   Pred. No. 1.6e-131;   Length 234;

RESULT 323
ID   ABM25368 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104541-A1.
PD   05-JUN-2003.

RESULT 324
ID   ABM19878 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030104554-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Pred. No. 1.6e-131;
Best Local Similarity   100.0%; Score 1195; DB 6; Length 234;

RESULT 325
ID   AB046784 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030049762-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Pred. No. 1.6e-131;
Best Local Similarity   100.0%; Score 1195; DB 6; Length 234;

RESULT 326
ID   AB047089 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030049765-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Pred. No. 1.6e-131;
Best Local Similarity   100.0%; Score 1195; DB 6; Length 234;

RESULT 327
ID   ADA83135 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030049752-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Pred. No. 1.6e-131;
Best Local Similarity   100.0%; Score 1195; DB 6; Length 234;

RESULT 328
ID   ABR71520 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030032133-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Pred. No. 1.6e-131;
Best Local Similarity   100.0%; Score 1195; DB 6; Length 234;

RESULT 329
ID   ABR72130 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030032136-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Pred. No. 1.6e-131;
Best Local Similarity   100.0%; Score 1195; DB 6; Length 234;

RESULT 330
ID   ABR98469 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030036129-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Pred. No. 1.6e-131;
Best Local Similarity   100.0%; Score 1195; DB 6; Length 234;

RESULT 331
ID   AB006839 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030040053-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Pred. No. 1.6e-131;
Best Local Similarity   100.0%; Score 1195; DB 6; Length 234;

RESULT 332
ID   ABR84792 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030040057-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Pred. No. 1.6e-131;
Best Local Similarity   100.0%; Score 1195; DB 6; Length 234;

RESULT 333
ID   ABR73350 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030054467-A1.
Query Match   100.0%; Pred. No. 1.6e-131;
Best Local Similarity   100.0%; Score 1195; DB 6; Length 234;

RESULT 334
ID   ABR76444 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030044932-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Pred. No. 1.6e-131;
Best Local Similarity   100.0%; Score 1195; DB 6; Length 234;

RESULT 335
ID   ABR73045 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030027270-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Pred. No. 1.6e-131;
Best Local Similarity   100.0%; Score 1195; DB 6; Length 234;

RESULT 336
ID   ABM1111 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030032126-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Pred. No. 1.6e-131;
Best Local Similarity   100.0%; Score 1195; DB 6; Length 234;

RESULT 337
ID   AB020570 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030054469-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Pred. No. 1.6e-131;
Best Local Similarity   100.0%; Score 1195; DB 6; Length 234;

RESULT 338
ID   AB025313 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030054466-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Pred. No. 1.6e-131;
Best Local Similarity   100.0%; Score 1195; DB 6; Length 234;

RESULT 339
ID   AB025618 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030059879-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Pred. No. 1.6e-131;
Best Local Similarity   100.0%; Score 1195; DB 6; Length 234;

RESULT 340
ID   ABR94027 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049738-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Pred. No. 1.6e-131;
Best Local Similarity   100.0%; Score 1195; DB 6; Length 234;

RESULT 341
ID   ABR79934 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030064469-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Pred. No. 1.6e-131;
Best Local Similarity   100.0%; Score 1195; DB 6; Length 234;

RESULT 342
ID   ABM11274 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.

RESULT 343

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ID   ABO32881 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030064453-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match   100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 344
ID   ABO30587 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein; 234 AA.
PN   US20030064466-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match   100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 345
ID   ABO30892 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030064468-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match   100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 346
ID   ABM27198 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068760-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match   100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 347
ID   ABM29943 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068769-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match   100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 348
ID   ABM05479 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030045700-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match   100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 349
ID   ABM15544 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068698-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match   100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 350
ID   ABM08529 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030049748-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match   100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 351
ID   ABO42229 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030064759-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match   100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 352
ID   ABO37959 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030068765-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match   100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 353
ID   ABO45869 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20030049754-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match   100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 354
ID   ABM66672 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068688-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match   100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 355
ID   ADB20178 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030082767-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match   100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 356
ID   ABM19573 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030104552-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match   100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 357
ID   ABO49285 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030049774-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match   100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 358
ID   ABO49590 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030049775-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match   100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 359
ID   ADA78430 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US20030073181-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match   100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 360
ID   ABR88147 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US20030068720-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match   100.0%;  Score 1195;  DB 6;  Length 234;
     Best Local Similarity   100.0%;  Pred. No. 1.6e-131;

RESULT 361
ID   ADA00345 standard; protein; 234 AA.
DE   Human secreted/transmembrane polypeptide PRO 1864.
PN   US20030027992-A1.
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PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;   Score 1195;  DB 6;   Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 362
ID   ABM26893 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068739-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;   Score 1195;  DB 6;   Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 363
ID   ABM03290 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068763-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;   Score 1195;  DB 6;   Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 364
ID   ABO39789 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068689-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;   Score 1195;  DB 6;   Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 365
ID   ABO49895 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049776-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;   Score 1195;  DB 7;   Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 366
ID   ABO50810 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049780-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;   Score 1195;  DB 7;   Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 367
ID   ABO05266 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003036126-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;   Score 1195;  DB 7;   Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 368
ID   ABR74570 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044924-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;   Score 1195;  DB 7;   Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 369
ID   ABR77049 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003044927-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;   Score 1195;  DB 7;   Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 370
ID   ABM17806 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040072-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;   Score 1195;  DB 7;   Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 371
ID   ABR95857 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003040073-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;   Score 1195;  DB 7;   Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 372
ID   ABO21790 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003032124-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;   Score 1195;  DB 7;   Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 373
ID   ABO19960 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003054467-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;   Score 1195;  DB 7;   Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 374
ID   ABO24263 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003054455-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;   Score 1195;  DB 7;   Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 375
ID   ABR86012 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049759-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;   Score 1195;  DB 7;   Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 376
ID   ABM10664 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064455-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;   Score 1195;  DB 7;   Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 377
ID   ABM76663 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003054465-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;   Score 1195;  DB 7;   Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 378
ID   ABR93367 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073170-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;   Score 1195;  DB 7;   Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 379
ID   ABM12494 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073176-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          100.0%;   Score 1195;  DB 7;   Length 234;
     Best Local Similarity 100.0%;  Pred. No. 1.6e-131;
RESULT 380
ID   ABM05784 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068717-A1.
PD   10-APR-2003.
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PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195;   DB 7;
     Best Local Similarity     100.0%;   Pred. No. 1.6e-131;   Length 234;
RESULT 381
ID   ABO34909 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068728-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195;   DB 7;
     Best Local Similarity     100.0%;   Pred. No. 1.6e-131;   Length 234;
RESULT 382
ID   ABM02985 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068764-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195;   DB 7;
     Best Local Similarity     100.0%;   Pred. No. 1.6e-131;   Length 234;
RESULT 383
ID   ABM18963 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104550-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195;   DB 7;
     Best Local Similarity     100.0%;   Pred. No. 1.6e-131;   Length 234;
RESULT 384
ID   ABM19268 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003104551-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195;   DB 7;
     Best Local Similarity     100.0%;   Pred. No. 1.6e-131;   Length 234;
RESULT 385
ID   ABO46479 standard; protein; 234 AA.
DE   Human PRO polypeptide.
PN   US2003049761-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195;   DB 7;
     Best Local Similarity     100.0%;   Pred. No. 1.6e-131;   Length 234;
RESULT 386
ID   ABO48980 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049757-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195;   DB 7;
     Best Local Similarity     100.0%;   Pred. No. 1.6e-131;   Length 234;
RESULT 387
ID   ABR69023 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003027273-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195;   DB 7;
     Best Local Similarity     100.0%;   Pred. No. 1.6e-131;   Length 234;
RESULT 388
ID   ABR89062 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036119-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195;   DB 7;
     Best Local Similarity     100.0%;   Pred. No. 1.6e-131;   Length 234;
RESULT 389
ID   ABR72435 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036120-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195;   DB 7;
     Best Local Similarity     100.0%;   Pred. No. 1.6e-131;   Length 234;
RESULT 390

ID   ABR74265 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003036161-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195;   DB 7;
     Best Local Similarity     100.0%;   Pred. No. 1.6e-131;   Length 234;
RESULT 391
ID   ABO18533 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003049739-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195;   DB 7;
     Best Local Similarity     100.0%;   Pred. No. 1.6e-131;   Length 234;
RESULT 392
ID   ABR80239 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003049921-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195;   DB 7;
     Best Local Similarity     100.0%;   Pred. No. 1.6e-131;   Length 234;
RESULT 393
ID   ABM01460 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003059882-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195;   DB 7;
     Best Local Similarity     100.0%;   Pred. No. 1.6e-131;   Length 234;
RESULT 394
ID   ABM02070 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003059884-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195;   DB 7;
     Best Local Similarity     100.0%;   Pred. No. 1.6e-131;   Length 234;
RESULT 395
ID   ABR87232 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003068687-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195;   DB 7;
     Best Local Similarity     100.0%;   Pred. No. 1.6e-131;   Length 234;
RESULT 396
ID   ABM12799 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003073186-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195;   DB 7;
     Best Local Similarity     100.0%;   Pred. No. 1.6e-131;   Length 234;
RESULT 397
ID   ABM30553 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064443-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195;   DB 7;
     Best Local Similarity     100.0%;   Pred. No. 1.6e-131;   Length 234;
RESULT 398
ID   ABM24453 standard; protein; 234 AA.
DE   Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN   US2003064444-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match               100.0%;   Score 1195;   DB 7;
     Best Local Similarity     100.0%;   Pred. No. 1.6e-131;   Length 234;
RESULT 399
ID   ABO29367 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
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PN US20030668697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

RESULT 400
ID ABO31197 standard; protein; 234 AA.
DE Human secreted/transmembrane protein; 234 AA.
PN US20030668710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

RESULT 401
ID ABM14324 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030668686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

RESULT 402
ID ABM09749 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030173178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

RESULT 403
ID ABO38874 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030668774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

RESULT 404
ID ABM34639 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030104538-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

RESULT 405
ID ABO51115 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

RESULT 406
ID ABO10411 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US20030035151-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

RESULT 407
ID ABO03941 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030036158-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

RESULT 408
ID ABR77654 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030040067-A1.
PD 27-FEB-2003.
Best Local Similarity 100.0%; Score 1195; Length 234;

RESULT 409
ID ABR78864 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030054456-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

RESULT 410
ID ABO23958 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

RESULT 411
ID ABR93722 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

RESULT 412
ID ABM01765 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030055983-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

RESULT 413
ID ABM78188 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

RESULT 414
ID ABR89977 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

RESULT 415
ID ABM27503 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

RESULT 416
ID ABM13104 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

RESULT 417
ID ABO31807 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

RESULT 418
ID ABM14019 standard; protein; 234 AA.

DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030668683-A1.
PD 10-APR-2003.

RESULT 419
Best Local Similarity
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

ID ABM08224 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030668754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

RESULT 420
Best Local Similarity
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

ID ABO40094 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030668681-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

RESULT 421
Best Local Similarity
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

ID ABM74529 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

RESULT 422
Best Local Similarity
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

ID ABM33724 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

RESULT 423
Best Local Similarity
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

ID ABM20183 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

RESULT 424
Best Local Similarity
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

ID ABO48675 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

RESULT 425
Best Local Similarity
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

ID ABR72740 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

RESULT 426
Best Local Similarity
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

ID ABO15382 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030036122-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

RESULT 427
Best Local Similarity
Query Match 100.0%; Pred. No. 1.6e-131;
Best Local Similarity 100.0%; Score 1195; DB 7; Length 234;

ID ABR85097 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 428
ID ABO15077 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 429
ID ABO17212 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030040077-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 430
ID ABM17501 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030044928-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 431
ID ABR85402 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 432
ID ABM76968 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 433
ID ABO28147 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 434
ID ABM22928 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030067757-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 435
ID ABM30248 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 436
ID ABM21708 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 437
ID ABM21403 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.

PN US20030068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 438
ID ABM14934 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 439
ID ABO41009 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 440
ID ABO36739 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 441
ID ABO07349 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 442
ID ABM75139 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 443
ID ABM33419 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 444
ID ABO46174 standard; protein; 234 AA.
PN US20030049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 445
ID ADA82501 standard; protein; 234 AA.
DE Human secreted/transmembrane protein #33.
PN US20030049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 446
ID ADB85587 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20030049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 447
ID ABM31773 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068880-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 448
ID ABM31163 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 449
ID ADB85809 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US20030054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 450
ID ABM32078 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 451
ID ABM32383 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 452
ID ADB68266 standard; protein; 234 AA.
DE Human PRO1864 protein.
PN US20030065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 453
ID ADB68073 standard; protein; 234 AA.
DE Human PRO1864 protein.
PN US20030060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 454
ID ABM31468 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity 100.0%; Pred. No. 1.6e-131;

RESULT 455
ID ABM30858 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US20030068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

RESULT 456
ID   ADB90890 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003083473-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 457
ID   ADC06970 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003060602-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 458
ID   ADC17149 standard; protein; 234 AA.
DE   Mammalian PRO polypeptide (SeqID 14).
PN   US2003065143-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 459
ID   ADC14847 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003073208-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 460
ID   ADC52342 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003138882-A1.
PD   24-JUL-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 461
ID   ADD05539 standard; protein; 234 AA.
DE   Human secreted and transmembrane protein (PRO) #33.
PN   US2003087376-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 462
ID   ADD10351 standard; protein; 234 AA.
DE   Human secreted and transmembrane PRO polypeptide #31.
PN   US2003105011-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 463
ID   ADD11311 standard; protein; 234 AA.
DE   Human secreted and transmembrane PRO polypeptide #31.
PN   US2003105013-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 464
ID   ADD37104 standard; protein; 234 AA.
DE   Human secreted and transmembrane PRO polypeptide #31.
PN   US2003105012-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 465
ID   ADD36018 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003105296-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 466
ID   ADG01019 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003078387-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 467
ID   ADG08572 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180793-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 468
ID   ADG02534 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003207397-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 469
ID   ADG01241 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003207399-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 470
ID   ADF95416 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003207398-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 471
ID   ADF95193 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180795-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 472
ID   ADG12231 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003207392-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 473
ID   ADH24046 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003180918-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 474

ID   ADH34072 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031809858-A1.
PN   US20031809858-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.

RESULT 475
ID   ADH29905 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031809859-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 476
ID   ADH23876 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031809919-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 477
ID   ADH08891 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003207395-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 478
ID   ADG85280 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031809904-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 479
ID   ADH24556 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031809907-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 480
ID   ADH37412 standard; protein; 234 AA.
DE   Human secreted and transmembrane protein PRO1864.
PN   US20031816646-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 481
ID   ADH02001 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US20031816648-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 482
ID   ADH37582 standard; protein; 234 AA.
DE   Human secreted and transmembrane protein PRO1864.
PN   US20031816648-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 483
ID   ADG85620 standard; protein; 234 AA.

DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031809905-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.

RESULT 484
ID   ADH24216 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031809914-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 485
ID   ADH38510 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031816643-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 486
ID   ADG83631 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US20031809794-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 487
ID   ADH29439 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031809860-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 488
ID   ADH27555 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031809906-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 489
ID   ADH37752 standard; protein; 234 AA.
DE   Human secreted and transmembrane protein PRO1864.
PN   US20031816647-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 490
ID   ADH37929 standard; protein; 234 AA.
DE   Human secreted and transmembrane protein PRO1864.
PN   US20031816649-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 491
ID   ADH57349 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031809920-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1195;   DB 7;   Length 234;
     Best Local Similarity 100.0%;   Pred. No. 1.6e-131;

RESULT 492
ID   ADH53491 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.

PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.6e-131;
RESULT 493
ID ADH53661 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.6e-131;
RESULT 494
ID ADH51997 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.6e-131;
RESULT 495
ID ADH49852 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.6e-131;
RESULT 496
ID ADI25362 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.6e-131;
RESULT 497
ID ADH90155 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.6e-131;
RESULT 498
ID ADI25532 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.6e-131;
RESULT 499
ID ADH97706 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.6e-131;
RESULT 500
ID ADI03554 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.6e-131;
RESULT 501
ID ADI11911 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181686-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.6e-131;
RESULT 502
ID ADH89985 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.6e-131;
RESULT 503
ID ADH98386 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.6e-131;
RESULT 504
ID ADI11061 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.6e-131;
RESULT 505
ID ADI11571 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.6e-131;
RESULT 506
ID ADH98216 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.6e-131;
RESULT 507
ID ADH98556 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.6e-131;
RESULT 508
ID ADH98046 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.6e-131;
RESULT 509
ID ADI05034 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%; Score 1195; DB 7; Length 234;
    Best Local Similarity   100.0%; Pred. No. 1.6e-131;
RESULT 510
ID ADI03384 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181654-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 511
ID ADI04779 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20031816557-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 512
ID ADH78233 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US20031816668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 513
ID ADI19577 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20031816676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 514
ID ADH90325 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20031816699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 515
ID ADI03044 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20031816653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 516
ID ADH77893 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US20031816666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 517
ID ADH97876 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20031816674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 518
ID ADI01261 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20031910669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 519
ID ADI01956 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20031911288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 520
ID ADI03214 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20031816555-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 521
ID ADI11401 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US20031816681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 522
ID ADI02303 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20031816650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 523
ID ADI11741 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US20031816685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 524
ID ADI05378 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20031910716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 525
ID ADH79450 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20031910290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 526
ID ADI11407 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20031816675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 527
ID ADI05208 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20031816677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
RESULT 528
ID ADH79620 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US20031191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195;

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Best Local Similarity    100.0%;   Pred. No. 1.6e-131;
RESULT 529
ID   ADI01446 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181678-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.6e-131;
RESULT 530
ID   ADI01616 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181679-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.6e-131;
RESULT 531
ID   ADI01786 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181680-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.6e-131;
RESULT 532
ID   ADH79790 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003191289-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.6e-131;
RESULT 533
ID   ADI04608 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003171550-A1.
PD   11-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.6e-131;
RESULT 534
ID   ADI02744 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181651-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.6e-131;
RESULT 535
ID   ADH78063 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US2003181667-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.6e-131;
RESULT 536
ID   ADI25702 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181670-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.6e-131;
RESULT 537
ID   ADI25872 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003181671-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.6e-131;

RESULT 538
ID   ADK65384 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003073821-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.6e-131;
RESULT 539
ID   ADH98726 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003191284-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.6e-131;
RESULT 540
ID   ADH79967 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003191287-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.6e-131;
RESULT 541
ID   ADI32672 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003207396-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.6e-131;
RESULT 542
ID   ADM30206 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003073813-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.6e-131;
RESULT 543
ID   ADL93698 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003040013-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;   Score 1195;  DB 7;  Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.6e-131;
RESULT 544
ID   ADC52152 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2003130483-A1.
PD   10-JUL-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;   Score 1195;  DB 8;  Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.6e-131;
RESULT 545
ID   ADE41312 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein PRO polypeptide #31.
PN   US2003100497-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;   Score 1195;  DB 8;  Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.6e-131;
RESULT 546
ID   ADE74203 standard; protein; 234 AA.
DE   Human secreted/transmembrane protein (PRO) #33.
PN   US2003211572-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match          100.0%;   Score 1195;  DB 8;  Length 234;
Best Local Similarity    100.0%;   Pred. No. 1.6e-131;
RESULT 547
ID   ADE74815 standard; protein; 234 AA.
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DE Human secreted/transmembrane protein (PRO) #33.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 548
ID ADF96028 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 549
ID ADG04299 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003215912-A1.
PD 20-NOV-2003.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 550
ID ADG00459 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003215911-A1.
PD 20-NOV-2003.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 551
ID ADH06584 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180852-A1.
PD 25-SEP-2003.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 552
ID ADH06414 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180853-A1.
PD 25-SEP-2003.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 553
ID ADG68835 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180855-A1.
PD 25-SEP-2003.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 554
ID ADH27725 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180912-A1.
PD 25-SEP-2003.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 555
ID ADH25066 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180913-A1.
PD 25-SEP-2003.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 556
ID ADH33698 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181645-A1.
PD 25-SEP-2003.

RESULT 557
ID ADG82715 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003215910-A1.
PD 20-NOV-2003.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 558
ID ADH02341 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180839-A1.
PD 25-SEP-2003.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 559
ID ADH07948 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180845-A1.
PD 25-SEP-2003.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 560
ID ADG69345 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180846-A1.
PD 25-SEP-2003.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 561
ID ADH39166 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180917-A1.
PD 25-SEP-2003.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 562
ID ADH25996 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003068770-A1.
PD 10-APR-2003.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 563
ID ADG83906 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003166848-A1.
PD 04-SEP-2003.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 564
ID ADG85450 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180842-A1.
PD 25-SEP-2003.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.6e-131;
PA (GETH) GENENTECH INC.

RESULT 565
ID ADH06244 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

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RESULT 566
ID   ADH30074 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20003180856-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 567
ID   ADH24386 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20003180910-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 568
ID   ADH32965 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US2003068768-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 569
ID   ADG69515 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20003180844-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 570
ID   ADH07778 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20003180851-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 571
ID   ADG85790 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20003180861-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 572
ID   ADH39336 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20003180916-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 573
ID   ADH33528 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US20003181637-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 574
ID   ADH33868 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US20003181644-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 575
ID   ADH01078 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US20003180838-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 576
ID   ADG69685 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20003180843-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 577
ID   ADH02171 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US20003180841-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 578
ID   ADG69175 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20003180847-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 579
ID   ADG85960 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20003180862-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 580
ID   ADH24896 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20003180909-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 581
ID   ADH39513 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20003180915-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 582
ID   ADH02511 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US20003180840-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 583
ID   ADG69005 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20003180849-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;
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RESULT 584
ID   ADH07608 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031800550-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 585
ID   ADG86130 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031800863-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 586
ID   ADH24726 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031800908-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 587
ID   ADH25774 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031800911-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 588
ID   ADH38340 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031800922-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 589
ID   ADH71179 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031801642-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 590
ID   ADH43495 standard; protein; 234 AA.
DE   Human PRO polypeptide #31.
PN   US20032224984-A1.
PD   04-DEC-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 591
ID   ADH52167 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031800921-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 592
ID   ADH49533 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031800857-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 593

ID   ADH90495 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031801700-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 594
ID   ADI11231 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US20031801683-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 595
ID   ADH98896 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031901698-A1.
PD   09-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 596
ID   ADI02126 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031901699-A1.
PD   09-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 597
ID   ADH90665 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031801701-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 598
ID   ADJ54704 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20040023321-A1.
PD   05-FEB-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 599
ID   ADJ98540 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031871197-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 600
ID   ADJ98710 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031871228-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 601
ID   ADH78869 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031801703-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity   100.0%; Pred. No. 1.6e-131;

RESULT 602
ID   ADJ99103 standard; protein; 234 AA.

DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031864008-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.

RESULT 603
ID   ADJ99273 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031871956-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 604
ID   ADJ98891 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031872421-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 605
ID   ADH79039 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20031817021-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 606
ID   ADK00899 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US20031864071-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 607
ID   ADK14420 standard; protein; 234 AA.
DE   Human PRO polypeptide #31.
PN   US20031872291-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 608
ID   ADK82840 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20040439271-A1.
PD   04-MAR-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 609
ID   ADJ64475 standard; protein; 234 AA.
DE   Human PRO polypeptide #33.
PN   US20040383371-A1.
PD   26-FEB-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 610
ID   ADM31371 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20040483341-A1.
PD   11-MAR-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 611
ID   ADM36181 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.

PN   US20040533581-A1.
PD   18-MAR-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 612
ID   ADM40223 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20040483351-A1.
PD   11-MAR-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 613
ID   ADM80869 standard; protein; 234 AA.
DE   Human PRO polypeptide #7.
PN   US20040584111-A1.
PD   25-MAR-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 614
ID   ADL91873 standard; protein; 234 AA.
DE   Human PRO1864 protein SEQ ID NO.94.
PN   WO200402407601-A2.
PD   25-MAR-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 615
ID   ADN37831 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US20040919591-A1.
PD   13-MAY-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 8;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 616
ID   ADY18016 standard; protein; 234 AA.
DE   PRO polypeptide SEQ ID NO 3822.
PN   WO200501696201-A2.
PD   24-FEB-2005.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 9;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 617
ID   ADY19397 standard; protein; 234 AA.
DE   PRO polypeptide SEQ ID NO 5203.
PN   WO200501696201-A2.
PD   24-FEB-2005.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1195;   DB 9;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 618
ID   ADY77709 standard; protein; 234 AA.
DE   Neoplastic disease detection protein PRO1864.
PN   US20050591021-A1.
PD   17-MAR-2005.
PA   (EATO/) EATON D L.
PA   (FILV/) FILVAROFF E.
PA   (GERK/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI J C.
PA   (GURN/) GURNEY A L.
PA   (WATA/) WATANABE C K.
PA   (WOOD/) WOOD W I.
Query Match   100.0%;   Score 1195;   DB 9;   Length 234;
Best Local Similarity   100.0%;   Pred. No. 1.6e-131;

RESULT 619
ID   AEA08359 standard; protein; 234 AA.
DE   Steriodogenic acute regulatory protein related (MLN64).
PN   WO200504753601-A2.

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PD   26-MAY-2005.
PA   (NOVS )  NOVARTIS AG.
PA   (NOVS )  NOVARTIS PHARMA GMBH.
RESULT 620
Best Local Similarity 100.0%;   Score 1195;  DB 9;   Length 234;
  Query Match      100.0%;   Pred. No. 1.6e-131;
ID   AEDS0061 standard; protein; 234 AA.
DE   Novel human secreted and transmembrane protein PRO1864.
PN   US2005163766-A1.
PD   28-JUL-2005.
PA   (HUMA-)
RESULT 621
Best Local Similarity 100.0%;   Score 1195;  DB 9;   Length 234;
  Query Match      100.0%;   Pred. No. 1.6e-131;
ID   AEF12540 standard; protein; 234 AA.
DE   Human PRO1864 protein SEQ ID NO:14.
PN   US20060008901-A1.
PD   12-JAN-2006.
PA   (GETH )  GENENTECH INC.
RESULT 622
Best Local Similarity 100.0%;   Score 1195;  DB 10;  Length 234;
  Query Match      100.0%;   Pred. No. 1.6e-131;
ID   AEF74229 standard; protein; 234 AA.
DE   Human PRO1864 protein SEQ ID NO:14.
PN   US2005260647-A1.
PD   24-NOV-2005.
PA   (EATO/)  EATON D. L.
PA   (FILV/)  FILVAROFF E.
PA   (GERR/)  GERRITSEN M. E.
PA   (GODD/)  GODDARD A.
PA   (GODO/)  GODOWSKI P. J.
PA   (GRIM/)  GRIMALDI J. C.
PA   (GURN/)  GURNEY A. L.
PA   (WATA/)  WATANABE C K.
PA   (WOOD/)  WOOD W. L.
RESULT 623
Best Local Similarity 100.0%;   Score 1195;  DB 10;  Length 234;
  Query Match      100.0%;   Pred. No. 1.6e-131;
ID   AAM41716 standard; protein; 238 AA.
DE   Human polypeptide SEQ ID NO 6647.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
RESULT 624
Best Local Similarity 100.0%;   Score 1195;  DB 4;   Length 238;
  Query Match      100.0%;   Pred. No. 1.7e-131;
ID   AAM41715 standard; protein; 238 AA.
DE   Human polypeptide SEQ ID NO 6646.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
RESULT 625
Best Local Similarity 100.0%;   Score 1195;  DB 4;   Length 238;
  Query Match      100.0%;   Pred. No. 1.7e-131;
ID   ABP75508 standard; protein; 238 AA.
DE   Human secretory polypeptide SPTM SEQ ID NO 692.
PN   WO200283876-A2.
PD   24-OCT-2002.
PA   (INCY-) INCYTE GENOMICS INC.
RESULT 626
Best Local Similarity 100.0%;   Score 1195;  DB 6;   Length 238;
  Query Match      100.0%;   Pred. No. 1.7e-131;
ID   ABR58404 standard; protein; 234 AA.
DE   Human NOV19b.
PN   WO200302423-A2.
PD   10-APR-2003.
PA   (CURA-) CURAGEN CORP.
RESULT 627
Best Local Similarity 99.6%;   Score 1188;  DB 6;   Length 234;
  Query Match      99.4%;   Pred. No. 1.1e-130;
ID   AAM39930 standard; protein; 216 AA.
DE   Human polypeptide SEQ ID NO 3075.
PN   WO200153312-A1.
PD   26-JUL-2001.

PA   (HYSE-) HYSEQ INC.
RESULT 628
Best Local Similarity 92.3%;   Score 1097;  DB 4;   Length 216;
  Query Match      91.8%;   Pred. No. 4.9e-120;
ID   ABB90287 standard; protein; 201 AA.
DE   Human polypeptide SEQ ID NO 2663.
PN   WO200190304-A2.
PD   29-NOV-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
RESULT 629
Best Local Similarity 85.7%;   Score 1024;  DB 5;   Length 201;
  Query Match      82.4%;   Pred. No. 1.7e-111;
ID   ABR58403 standard; protein; 198 AA.
DE   Human NOV19a.
PN   WO200302423-A2.
PD   10-APR-2003.
PA   (CURA-) CURAGEN CORP.
RESULT 630
Best Local Similarity 84.6%;   Score 985;  DB 6;   Length 198;
  Query Match      82.4%;   Pred. No. 6.5e-107;
ID   AAU30250 standard; protein; 283 AA.
DE   Novel human secreted protein #741.
PN   WO200179449-A2.
PD   25-OCT-2001.
PA   (CURA-) CURAGEN CORP.
RESULT 631
Best Local Similarity 72.5%;   Score 777;  DB 4;   Length 283;
  Query Match      65.0%;   Pred. No. 3.2e-82;
ID   ADB64413 standard; protein; 176 AA.
DE   Human protein encoded by clone FEBRA20007820.
PN   EP1308459-A2.
PD   07-MAY-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
RESULT 632
Best Local Similarity 87.5%;   Score 669.5;  DB 7;   Length 176;
  Query Match      56.0%;   Pred. No. 7.2e-70;
ID   ADK36828 standard; protein; 146 AA.
DE   Novel human polypeptide SeqID8910.
PN   WO200216439-A2.
PD   28-FEB-2002.
PA   (HYSE-) HYSEQ INC.
RESULT 633
Best Local Similarity 91.0%;   Score 665;  DB 5;   Length 146;
  Query Match      55.6%;   Pred. No. 1.9e-69;
ID   ADZ88813 standard; protein; 383 AA.
DE   Breast specific protein SEQ ID NO 180.
PN   WO200504075-A2.
PD   19-MAY-2005.
PA   (DIAD-) DIADEXUS INC.
RESULT 634
Best Local Similarity 56.2%;   Score 664;  DB 9;   Length 383;
  Query Match      55.6%;   Pred. No. 9.4e-69;
ID   AAW25768 standard; protein; 445 AA.
DE   Human MLN 64.
PN   WO9706256-A2.
PD   20-FEB-1997.
PA   (INRM ) INST NAT SANTE & RECH MEDICALE.
PA   (CNRS ) CENT NAT RECH SCI.
PA   (UYPA-) UNIV PASTEUR LOUIS.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
RESULT 635
Best Local Similarity 56.2%;   Score 664;  DB 2;   Length 445;
  Query Match      55.6%;   Pred. No. 1.2e-68;
ID   ABR47530 standard; protein; 445 AA.
DE   Breast cancer associated protein sequence SEQ ID NO:296.
PN   WO200304989-A2.
PD   16-JAN-2003.
PA   (MILL-) MILLENIUM PHARM INC.
RESULT 636
Best Local Similarity 56.2%;   Score 664;  DB 6;   Length 445;
  Query Match      55.6%;   Pred. No. 2.6e-68;
ID   ADH13184 standard; protein; 445 AA.
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DE Human malignant neoplasia-related protein seqID33.
PN EP1365034-A2.
PD 26-NOV-2003.
PA (FARB) BAYER AG.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 55.6%;
Best Local Similarity 56.2%; Score 664; DB 8; Length 445;
Pred. No. 1.2e-68;

RESULT 637
ID AEA15071 standard; protein; 445 AA.
DE Human polypeptide #7.
PN WO200504753A-A2.
PD 26-MAY-2005.
PA (DIAD-) DIADEXUS INC.
Query Match 55.6%;
Best Local Similarity 56.2%; Score 664; DB 9; Length 445;
Pred. No. 1.2e-68;

RESULT 638
ID ADZ88812 standard; protein; 497 AA.
DE Breast specific protein SEQ ID NO 179.
PN WO2005044075-A2.
PD 19-MAY-2005.
PA (HYSE-) HYSEQ INC.
Query Match 55.6%;
Best Local Similarity 56.2%; Score 664; DB 9; Length 497;
Pred. No. 1.4e-68;

RESULT 639
ID ABG05498 standard; protein; 534 AA.
DE Novel human diagnostic protein #5489.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (DIAD-) DIADEXUS INC.
Query Match 52.3%;
Best Local Similarity 52.3%; Score 625; DB 9; Length 534;
Pred. No. 5.8e-64;

RESULT 640
ID ABR69622 standard; protein; 412 AA.
DE Human CGDD-22 protein.
PN WO2003027263-A2.
PD 03-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 58.3%;
Best Local Similarity 48.9%; Score 578; DB 6; Length 412;
Pred. No. 1.4e-58;

RESULT 641
ID ABP75900 standard; protein; 111 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 1084.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 73.7%;
Best Local Similarity 48.4%; Score 405.5; DB 6; Length 111;
Pred. No. 4.4e-39;

RESULT 642
ID ABS59968 standard; protein; 580 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6696.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 37.8%;
Best Local Similarity 33.9%; Score 343; DB 4; Length 580;
Pred. No. 9.7e-31;

RESULT 643
ID AAM90384 standard; protein; 70 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:17977.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 37.8%;
Best Local Similarity 28.7%; Score 322; DB 4; Length 70;
Pred. No. 1.5e-29;

RESULT 644
ID AAB96837 standard; protein; 424 AA.
DE Putative P. abyssi nucleoside-diphosphate-sugar pyrophosphorylase #6.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 98.4%;
Best Local Similarity 26.9%; Score 93.5; DB 4; Length 424;
Pred. No. 0.14;

RESULT 645
ID AAU03699 standard; protein; 373 AA.
Query Match 7.8%;
Best Local Similarity 21.9%; Score 91; DB 4; Length 373;
DE Group B Streptococcus antigenic protein, ID-176.
PN WO200132882-A2.
PD 10-MAY-2001.
PA (MICR-) MICROBIAL TECHNICS LTD.
Query Match 7.6%;
Best Local Similarity 25.7%; Score 91; DB 4; Length 373;
Pred. No. 0.23;

RESULT 646
ID ADV89705 standard; protein; 605 AA.
DE Streptococcus agalactiae protein; 605 AA.
PN FR2824074-A1.
PD 31-OCT-2002.
PA (CNRS) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI
Query Match 7.6%;
Best Local Similarity 25.7%; Score 91; DB 8; Length 605;
Pred. No. 0.46;

RESULT 647
ID ADV80958 standard; protein; 605 AA.
DE Streptococcus agalactiae protein sequence, SEQ ID 2099.
PN WO200292818-A2.
PD 21-NOV-2002.
PA (CNRS) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI
Query Match 7.6%;
Best Local Similarity 25.7%; Score 91; DB 8; Length 605;
Pred. No. 0.46;

RESULT 648
ID ABP30317 standard; protein; 651 AA.
DE Streptococcus agalactiae protein, SEQ ID 9810.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 7.6%;
Best Local Similarity 25.7%; Score 91; DB 5; Length 651;
Pred. No. 0.5;

RESULT 649
ID ADV83104 standard; protein; 651 AA.
DE Streptococcus agalactiae protein, SEQ ID 4245.
PN WO200292818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI
Query Match 7.6%;
Best Local Similarity 25.7%; Score 91; DB 8; Length 651;
Pred. No. 0.5;

RESULT 650
ID ABP29732 standard; protein; 654 AA.
DE Streptococcus polypeptide SEQ ID NO 8640.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 7.6%;
Best Local Similarity 25.7%; Score 91; DB 5; Length 654;
Pred. No. 0.51;

RESULT 651
ID ABP26469 standard; protein; 654 AA.
DE Streptococcus polypeptide SEQ ID NO 2114.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 7.6%;
Best Local Similarity 25.7%; Score 91; DB 5; Length 654;
Pred. No. 0.51;

RESULT 652
ID AAG61678 standard; protein; 155 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 80037.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.3%;
Best Local Similarity 21.4%; Score 87.5; DB 3; Length 155;
Pred. No. 0.18;

RESULT 653
ID AAG59838 standard; protein; 155 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77441.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.3%;
Best Local Similarity 21.4%; Score 87.5; DB 3; Length 155;
Pred. No. 0.18;

RESULT 654
ID   AAB58945 standard; protein; 516 AA.
DE   Breast and ovarian cancer associated antigen protein sequence SEQ ID 653.
PN   WO200055173-A1.
PD   21-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   21.4%;   Pred. No. 0.18;
Best Local Similarity   25.2%;   Score 87.5;   DB 3;   Length 516;

RESULT 655
ID   ADQ39266 standard; protein; 421 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 929.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
Query Match   7.3%;   Pred. No. 0.94;
Best Local Similarity   23.7%;   Score 87;   DB 8;   Length 421;

RESULT 656
ID   ADQ39263 standard; protein; 223 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 926.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
Query Match   7.3%;   Pred. No. 0.81;
Best Local Similarity   25.5%;   Score 85.5;   DB 8;   Length 223;

RESULT 657
ID   ADQ39258 standard; protein; 285 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 925.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
Query Match   7.2%;   Pred. No. 0.51;
Best Local Similarity   25.5%;   Score 85.5;   DB 8;   Length 285;

RESULT 658
ID   ADQ39262 standard; protein; 315 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 921.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
Query Match   7.2%;   Pred. No. 0.71;
Best Local Similarity   25.5%;   Score 85.5;   DB 8;   Length 315;

RESULT 659
ID   ADQ39260 standard; protein; 323 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 923.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
Query Match   7.2%;   Pred. No. 0.82;
Best Local Similarity   25.5%;   Score 85.5;   DB 8;   Length 323;

RESULT 660
ID   ADQ39261 standard; protein; 328 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 924.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
Query Match   7.2%;   Pred. No. 0.85;
Best Local Similarity   25.5%;   Score 85.5;   DB 8;   Length 328;

RESULT 661
ID   ADQ39265 standard; protein; 338 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 928.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
Query Match   7.2%;   Pred. No. 0.86;
Best Local Similarity   25.5%;   Score 85.5;   DB 8;   Length 338;

RESULT 662
ID   ADQ39267 standard; protein; 339 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 930.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
Query Match   7.2%;   Pred. No. 0.9;
Best Local Similarity   25.5%;   Score 85.5;   DB 8;   Length 339;

RESULT 663
ID   ADE28099 standard; protein; 340 AA.
DE   Human NTRAN protein - SEQ ID 4.
PN   WO2003051902-A1.
PD   26-JUN-2003.
PA   (INCY-) INCYTE GENOMICS INC.
Query Match   7.2%;   Pred. No. 0.91;
Best Local Similarity   25.5%;   Score 85.5;   DB 7;   Length 340;

RESULT 664
ID   ADQ39269 standard; protein; 384 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 932.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
Query Match   7.2%;   Pred. No. 1.1;
Best Local Similarity   25.5%;   Score 85.5;   DB 8;   Length 384;

RESULT 665
ID   ADQ39264 standard; protein; 390 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 927.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
Query Match   7.2%;   Pred. No. 1.1;
Best Local Similarity   25.5%;   Score 85.5;   DB 8;   Length 390;

RESULT 666
ID   ABU26680 standard; protein; 396 AA.
DE   Protein encoded by Prokaryotic essential gene #12207.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   7.2%;   Pred. No. 1.1;
Best Local Similarity   21.0%;   Score 85.5;   DB 6;   Length 396;

RESULT 667
ID   AAW13575 standard; protein; 438 AA.
DE   Batten disease polypeptide CLN3.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
Query Match   7.2%;   Pred. No. 1.3;
Best Local Similarity   25.5%;   Score 85.5;   DB 2;   Length 438;

RESULT 668
ID   AAW13589 standard; protein; 438 AA.
DE   Batten disease CLN3 mutant protein in family L204.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
Query Match   7.2%;   Pred. No. 1.3;
Best Local Similarity   25.5%;   Score 85.5;   DB 2;   Length 438;

RESULT 669
ID   AAW13582 standard; protein; 438 AA.
DE   Batten disease CLN3 mutant protein in family L46.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
Query Match   7.2%;   Pred. No. 1.3;
Best Local Similarity   24.8%;   Score 85.5;   DB 2;   Length 438;

RESULT 670
ID   AAW13577 standard; protein; 438 AA.
DE   Batten disease CLN3 mutant protein in family L39.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.
Query Match   7.2%;   Pred. No. 1.3;
Best Local Similarity   25.5%;   Score 85.5;   DB 2;   Length 438;

RESULT 671
ID   ADQ96392 standard; protein; 438 AA.
DE   T cell activation associated protein #285.
PN   WO2004058805-A2.
PD   15-JUL-2004.
Query Match   7.2%;   Pred. No. 1.3;
Best Local Similarity   25.5%;   Score 85.5;   DB 2;   Length 438;

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PA   (ASAH-) ASAHI KASEI PHARMA CORP.
     Query Match        7.2%;   Score 85.5;   DB 8;   Length 438;
     Best Local Similarity  25.5%;   Pred. No. 1.3;
RESULT 672
ID   ADQ39268 standard; protein; 438 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 931.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (CURA-) CURAGEN CORP.
PA   (APPL-) APPLERA CORP.

     Query Match        7.2%;   Score 85.5;   DB 8;   Length 438;
     Best Local Similarity  25.5%;   Pred. No. 1.3;
RESULT 673
ID   ADA05822 standard; protein; 440 AA.
DE   Human NOV43a protein SEQ ID NO:182.
PN   WO2003029424-A2.
PD   10-APR-2003.
PA   (CURA-) CURAGEN CORP.

     Query Match        7.2%;   Score 85.5;   DB 6;   Length 440;
     Best Local Similarity  25.2%;   Pred. No. 1.3;
RESULT 674
ID   ADN63244 standard; protein; 440 AA.
DE   Human NOV43a variant.
PN   US2004038223-A1.
PD   26-FEB-2004.
PA   (SMIT/) SMITHSON G.
PA   (MILL/) MILLET I.
PA   (PEYM/) PEYMAN J A.
PA   (KEKU/) KEKUDA R.
PA   (JUJJ/) JU J.
PA   (LILL/) LI L.
PA   (GUOX/) GUO X.
PA   (PATT/) PATTURAJAN M.
PA   (SPYT/) SPYTEK K A.
PA   (EDIN/) EDINGER S R.
PA   (ELLE/) ELLERMAN K.
PA   (MALY/) MALYANKAR U M.
PA   (ORTT/) ORT T.
PA   (GORM/) GORMAN L.
PA   (ZERH/) ZERHUSEN B D.
PA   (ANDE/) ANDERSON D W.
PA   (ZHON/) ZHONG M.
PA   (CATT/) CATTERTON E.
PA   (JIWW/) JI W.
PA   (MILL/) MILLER C E.
PA   (RAST/) RASTELLI L.
PA   (STON/) STONE D J.
PA   (PENA/) PENA C E A.
PA   (SHEN/) SHENOY S G.
PA   (SHIM/) SHIMKETS R A.
PA   (ROTH/) ROTHENBERG M E.
PA   (LEAC/) LEACH M D.
PA   (AGEE/) AGEE M L.
PA   (BERG/) BERGHS C.
PA   (DIPI/) DIPIPPO V A.
PA   (EISE/) EISEN A.
PA   (GANG/) GANGOLLI E A.
PA   (RIEG/) RIEGER D K.
PA   (SPAD/) SPADERNA S K.

     Query Match        7.2%;   Score 85.5;   DB 8;   Length 440;
     Best Local Similarity  25.2%;   Pred. No. 1.3;
RESULT 675
ID   ADN62985 standard; protein; 440 AA.
DE   Human NOV43a.
PN   US2004038223-A1.
PD   26-FEB-2004.
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PA   (SPYT/) SPYTEK K A.
PA   (EDIN/) EDINGER S R.
PA   (ELLE/) ELLERMAN K.
PA   (MALY/) MALYANKAR U M.
PA   (ORTT/) ORT T.
PA   (GORM/) GORMAN L.
PA   (ZERH/) ZERHUSEN B D.
PA   (ANDE/) ANDERSON D W.
PA   (ZHON/) ZHONG M.
PA   (CATT/) CATTERTON E.
PA   (JIWW/) JI W.
PA   (MILL/) MILLER C E.
PA   (RAST/) RASTELLI L.
PA   (STON/) STONE D J.
PA   (PENA/) PENA C E A.
PA   (SHEN/) SHENOY S G.
PA   (SHIM/) SHIMKETS R A.
PA   (ROTH/) ROTHENBERG M E.
PA   (LEAC/) LEACH M D.
PA   (AGEE/) AGEE M L.
PA   (BERG/) BERGHS C.
PA   (DIPI/) DIPIPPO V A.
PA   (EISE/) EISEN A.
PA   (GANG/) GANGOLLI E A.
PA   (RIEG/) RIEGER D K.
PA   (SPAD/) SPADERNA S K.

     Query Match        7.2%;   Score 85.5;   DB 8;   Length 440;
     Best Local Similarity  25.2%;   Pred. No. 1.3;
RESULT 676
ID   AED74247 standard; protein; 449 AA.
DE   Human placental protein SEQ ID NO:1075.
PN   US2005255114-A1.
PD   17-NOV-2005.
PA   (NUVE-) NUVELO INC.

     Query Match        7.2%;   Score 85.5;   DB 9;   Length 449;
     Best Local Similarity  25.5%;   Pred. No. 1.3;
RESULT 677
ID   AAW13593 standard; protein; 467 AA.
DE   Batten disease CLN3 mutant protein in family L61.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (UYLE-) RIJKSUNIV LEIDEN.

     Query Match        7.2%;   Score 85.5;   DB 2;   Length 467;
     Best Local Similarity  25.5%;   Pred. No. 1.3;
RESULT 678
ID   ABB89640 standard; protein; 473 AA.
DE   Human polypeptide SEQ ID NO 2016.
PN   WO200190304-A2.
PD   29-NOV-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.

     Query Match        7.2%;   Score 85.5;   DB 5;   Length 473;
     Best Local Similarity  25.2%;   Pred. No. 1.4;
RESULT 679
ID   ADQ18055 standard; protein; 473 AA.
DE   Human soft tissue sarcoma-upregulated protein - SEQ ID 872.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.

     Query Match        7.2%;   Score 85.5;   DB 8;   Length 473;
     Best Local Similarity  25.2%;   Pred. No. 1.4;
RESULT 680
ID   ADU06406 standard; protein; 473 AA.
DE   Novel bronchial cancer-associated human protein SeqID630.
PN   DE10316701-A1.
PD   04-NOV-2004.
PA   (HINZ/) HINZMANN B.
PA   (HERM/) HERMANN K.
PA   (CAST/) HEIDEN CASTANOS-VELEZ E.

     Query Match        7.2%;   Score 85.5;   DB 8;   Length 473;
     Best Local Similarity  25.2%;   Pred. No. 1.4;
RESULT 681
ID   ADY20253 standard; protein; 473 AA.
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DE  PRO polypeptide SEQ ID NO 6059.
PN  WO200501962-A2.
PD  24-FEB-2005.
PA  (GETH) GENENTECH INC.
      Best Local Similarity    25.2%;
      Query Match    7.2%;    Score 85.5;  DB 9;  Length 473;

RESULT 682
ID  ABU40544 standard; protein; 500 AA.
DE  Protein encoded by Prokaryotic essential gene #26071.
PN  WO200277183-A2.
PD  03-OCT-2002.
PA  (ELIT-) ELITRA PHARM INC.
      Best Local Similarity    26.0%;
      Query Match    7.2%;    Score 85.5;  DB 6;  Length 500;

RESULT 683
ID  ADY09432 standard; protein; 527 AA.
DE  Plant full length insert polypeptide seqid 65247.
PN  US2004034888-A1.
PD  19-FEB-2004.
PA  (LIUJ/) LIU J.
PA  (ZHOU/) ZHOU Y.
PA  (KOVA/) KOVALIC D K.
PA  (SCRE/) SCREEN S E.
PA  (TABA/) TABASKA J E.
PA  (CAOY/) CAO Y.
      Best Local Similarity    17.6%;
      Query Match    7.1%;    Score 84.5;  DB 8;  Length 527;

RESULT 684
ID  ABU33210 standard; protein; 430 AA.
DE  Protein encoded by Prokaryotic essential gene #18737.
PN  WO200277183-A2.
PD  03-OCT-2002.
PA  (ELIT-) ELITRA PHARM INC.
      Best Local Similarity    25.5%;
      Query Match    7.1%;    Score 84.5;  DB 6;  Length 430;

RESULT 685
ID  AAW13588 standard; protein; 438 AA.
DE  Batten disease CLN3 mutant protein in family L10.
PN  WO9708308-A1.
PD  06-MAR-1997.
PA  (UYLE-) RIJKSUNIV LEIDEN.
      Best Local Similarity    24.8%;
      Query Match    7.1%;    Score 84.5;  DB 2;  Length 438;

RESULT 686
ID  AAG16921 standard; protein; 322 AA.
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 17749.
PN  EP1033405-A2.
PD  06-SEP-2000.
      Best Local Similarity    33.7%;
      Query Match    7.0%;    Score 83.5;  DB 3;  Length 322;

RESULT 687
ID  ABG22285 standard; protein; 472 AA.
DE  Novel human diagnostic protein #21276.
PN  WO200175067-A2.
PD  11-OCT-2001.
PA  (HYSE-) HYSEQ INC.
      Best Local Similarity    20.1%;
      Query Match    7.0%;    Score 83.5;  DB 4;  Length 472;

RESULT 688
ID  ABU35608 standard; protein; 239 AA.
DE  Protein encoded by Prokaryotic essential gene #21135.
PN  WO200277183-A2.
PD  03-OCT-2002.
PA  (ELIT-) ELITRA PHARM INC.
      Best Local Similarity    21.7%;
      Query Match    6.9%;    Score 82.5;  DB 6;  Length 239;

RESULT 689
ID  ADU22550 standard; protein; 389 AA.
DE  L. acidophilus cell surface protein homologue #63.
PN  WO200409692-A2.
PD  11-NOV-2004.
PA  (UYNC-) UNIV NORTH CAROLINA STATE.
      Best Local Similarity    24.7%;
      Query Match    6.9%;    Score 82.5;  DB 8;  Length 389;

RESULT 690
ID  AAW13590 standard; protein; 438 AA.
DE  Batten disease CLN3 mutant protein in family L216.
PN  WO9708308-A1.
PD  06-MAR-1997.
PA  (UYLE-) RIJKSUNIV LEIDEN.
      Best Local Similarity    19.5%;
      Query Match    6.9%;    Score 82.5;  DB 2;  Length 438;

RESULT 691
ID  ADB85263 standard; protein; 589 AA.
DE  Mouse RNAi homologue SEQ ID NO:144.
PN  EP1284297-A2.
PD  19-FEB-2003.
PA  (WARN ) WARNER LAMBERT CO.
      Best Local Similarity    19.5%;
      Query Match    6.9%;    Score 82.5;  DB 7;  Length 589;

RESULT 692
ID  ADX74800 standard; protein; 264 AA.
DE  Plant full length insert polypeptide seqid 44166.
PN  US2004034888-A1.
PD  19-FEB-2004.
PA  (LIUJ/) LIU J.
PA  (ZHOU/) ZHOU Y.
PA  (KOVA/) KOVALIC D K.
PA  (SCRE/) SCREEN S E.
PA  (TABA/) TABASKA J E.
PA  (CAOY/) CAO Y.
      Best Local Similarity    33.3%;
      Query Match    6.8%;    Score 81.5;  DB 8;  Length 264;

RESULT 693
ID  AAW13586 standard; protein; 438 AA.
DE  Batten disease CLN3 mutant protein in family L285.
PN  WO9708308-A1.
PD  06-MAR-1997.
PA  (UYLE-) RIJKSUNIV LEIDEN.
      Best Local Similarity    24.8%;
      Query Match    6.8%;    Score 81.5;  DB 2;  Length 438;

RESULT 694
ID  AAB92924 standard; protein; 519 AA.
DE  Human protein sequence SEQ ID NO:11574.
PN  EP1074617-A2.
PD  07-FEB-2001.
PA  (HELI-) HELIX RES INST.
      Best Local Similarity    22.6%;
      Query Match    6.8%;    Score 81.5;  DB 4;  Length 519;

RESULT 695
ID  ADE28193 standard; protein; 577 AA.
DE  Human MDDT protein - SEQ ID 43.
PN  WO2003046152-A2.
PD  05-JUN-2003.
PA  (INCY-) INCYTE GENOMICS INC.
      Best Local Similarity    22.6%;
      Query Match    6.8%;    Score 81.5;  DB 7;  Length 577;

RESULT 696
ID  ADN23155 standard; protein; 529 AA.
DE  Bacterial polypeptide #5808.
PN  US2003233675-A1.
PD  18-DEC-2003.
PA  (CAOY/) CAO Y.
PA  (HINK/) HINKLE G J.
PA  (SLAT/) SLATER S C.
PA  (CHEN/) CHEN X.
PA  (GOLD/) GOLDMAN B S.
      Best Local Similarity    23.1%;
      Query Match    6.8%;    Score 81;  DB 8;  Length 529;

RESULT 697
ID  ADN23156 standard; protein; 529 AA.
DE  Bacterial polypeptide #5809.
PN  US2003233675-A1.
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PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.

     Query Match             6.8%;  Score 81;  DB 8;  Length 529;
     Best Local Similarity  23.1%;  Pred. No. 5.7;
RESULT 698
ID   AAG53771 standard; protein; 322 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 68491.
PN   EP1033405-A2.
PD   06-SEP-2000.

     Query Match             6.7%;  Score 80.5;  DB 3;  Length 322;
     Best Local Similarity  32.7%;  Pred. No. 3.3;
RESULT 699
ID   AAG25639 standard; protein; 322 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 29783.
PN   EP1033405-A2.
PD   06-SEP-2000.

     Query Match             6.7%;  Score 80.5;  DB 3;  Length 322;
     Best Local Similarity  32.7%;  Pred. No. 3.3;
RESULT 700
ID   AAG53746 standard; protein; 322 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 68457.
PN   EP1033405-A2.
PD   06-SEP-2000.

     Query Match             6.7%;  Score 80.5;  DB 3;  Length 322;
     Best Local Similarity  32.7%;  Pred. No. 3.3;
RESULT 701
ID   AB061194 standard; protein; 350 AA.
DE   Klebsiella pneumoniae polypeptide seqid 9711.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.

     Query Match             6.7%;  Score 80.5;  DB 7;  Length 350;
     Best Local Similarity  31.8%;  Pred. No. 3.7;
RESULT 702
ID   ABB48552 standard; protein; 463 AA.
DE   Listeria monocytogenes protein #1256.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP ) INST. PASTEUR.

     Query Match             6.7%;  Score 80.5;  DB 5;  Length 463;
     Best Local Similarity  19.0%;  Pred. No. 5.4;
RESULT 703
ID   ABU33036 standard; protein; 463 AA.
DE   Protein encoded by Prokaryotic essential gene #18563.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.

     Query Match             6.7%;  Score 80.5;  DB 6;  Length 463;
     Best Local Similarity  19.0%;  Pred. No. 5.4;
RESULT 704
ID   ADD43870 standard; protein; 536 AA.
DE   Chlamydia trachomatis immunogenic protein, SEQ ID No 165.
PN   WO2003049762-A2.
PD   19-JUN-2003.
PA   (CHIR-) CHIRON SPA.
PA   (RATT/) RATTI G.
PA   (GRAN/) GRANDI G.

     Query Match             6.7%;  Score 80.5;  DB 7;  Length 536;
     Best Local Similarity  25.2%;  Pred. No. 6.6;
RESULT 705
ID   AEA19162 standard; protein; 536 AA.
DE   Chlamydia trachomatis protein - SEQ ID 165.
PN   US2005106162-A1.
PD   19-MAY-2005.
PA   (RATT/) RATTI G.
PA   (GRAN/) GRANDI G.

     Query Match             6.7%;  Score 80.5;  DB 9;  Length 536;
     Best Local Similarity  25.2%;  Pred. No. 6.6;
RESULT 706
ID   ADC42920 standard; protein; 891 AA.
DE   Vaccinia Virus Major Core protein P4a precursor.


PN   WO2003017943-A2.
PD   06-MAR-2003.
PA   (MYRI-) MYRIAD GENETICS INC.

     Query Match             6.7%;  Score 80.5;  DB 7;  Length 891;
     Best Local Similarity  23.3%;  Pred. No. 13;
RESULT 707
ID   ABB92830 standard; protein; 1780 AA.
DE   Herbicidally active polypeptide SEQ ID NO 2041.
PN   WO200210210-A2.
PD   07-FEB-2002.
PA   (BAYE ) BAYER AG.

     Query Match             6.7%;  Score 80.5;  DB 5;  Length 1780;
     Best Local Similarity  20.8%;  Pred. No. 35;
RESULT 708
ID   AEB31016 standard; protein; 1780 AA.
DE   Arabidopsis thaliana glucan synthase-like protein-5.
PN   WO2005111215-A2.
PD   24-NOV-2005.
PA   (BADI ) BASF PLANT SCI GMBH.

     Query Match             6.7%;  Score 80.5;  DB 9;  Length 1780;
     Best Local Similarity  20.8%;  Pred. No. 35;
RESULT 709
ID   AAB54399 standard; protein; 144 AA.
DE   Human pancreatic cancer antigen protein sequence SEQ ID NO:851.
PN   WO200055320-A1.
PD   21-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.

     Query Match             6.7%;  Score 80.5;  DB 3;  Length 144;
     Best Local Similarity  25.4%;  Pred. No. 1.2;
RESULT 710
ID   AAM39952 standard; protein; 238 AA.
DE   Human polypeptide SEQ ID NO 3097.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.

     Query Match             6.7%;  Score 80;  DB 3;  Length 238;
     Best Local Similarity  22.5%;  Pred. No. 2.5;
RESULT 711
ID   ADM04473 standard; protein; 238 AA.
DE   Human protein of the invention SEQ ID NO:3158.
PN   EP1347046-A1.
PD   24-SEP-2003.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.

     Query Match             6.7%;  Score 80;  DB 7;  Length 238;
     Best Local Similarity  22.5%;  Pred. No. 2.5;
RESULT 712
ID   AEC87403 standard; protein; 238 AA.
DE   Human cDNA clone protein D90ST20002780, SEQ ID 3158.
PN   EP1580263-A1.
PD   28-SEP-2005.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.

     Query Match             6.7%;  Score 80;  DB 9;  Length 238;
     Best Local Similarity  22.5%;  Pred. No. 2.5;
RESULT 713
ID   AAM41738 standard; protein; 249 AA.
DE   Human polypeptide SEQ ID NO 6669.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.

     Query Match             6.7%;  Score 80;  DB 4;  Length 249;
     Best Local Similarity  22.5%;  Pred. No. 2.6;
RESULT 714
ID   AAR77844 standard; protein; 309 AA.
DE   Molasses toxicity resistance protein RTM1.
PN   WO9514774-A2.
PD   01-JUN-1995.
PA   (CNRS ) CENT NAT RECH SCI.

     Query Match             6.7%;  Score 80;  DB 2;  Length 309;
     Best Local Similarity  28.0%;  Pred. No. 3.5;
RESULT 715
ID   ABM67388 standard; protein; 330 AA.
DE   Photorhabdus luminescens protein sequence #485.
PN   WO200294867-A2.
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PD   28-NOV-2002.
PA   (INSP) INST PASTEUR.
PA   (CNRS) CNRS CENT NAT RECH SCI.
  Query Match
  Best Local Similarity   24.6%;   Score 80;   DB 6;   Length 330;
RESULT 716
ID   AAE05831 standard; protein; 360 AA.
DE   Human gene 14 encoded secreted protein HDQFN31, SEQ ID NO: 77.
PN   WO200136440-A1.
PD   25-MAY-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Best Local Similarity   22.5%;   Score 80;   DB 4;   Length 360;
RESULT 717
ID   ABG64559 standard; protein; 360 AA.
DE   Human albumin fusion protein #1234.
PN   WO200177137-A1.
PD   18-OCT-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match
  Best Local Similarity   22.5%;   Score 80;   DB 5;   Length 360;
RESULT 718
ID   ADL77826 standard; protein; 360 AA.
DE   Albumin fusion protein related therapeutic protein X, SEQ ID No 1308.
PN   US200401013-A1.
PD   15-JAN-2004.
PA   (ROSE/) ROSEN C A.
PA   (HASE/) HASELTINE W A.
  Query Match
  Best Local Similarity   22.5%;   Score 80;   DB 8;   Length 360;
RESULT 719
ID   ADX66260 standard; protein; 516 AA.
DE   Plant full length insert polypeptide seqid 37103.
PN   US200403488-A1.
PD   19-FEB-2004.
  Best Local Similarity   20.0%;   Score 80;   DB 8;   Length 516;
RESULT 720
ID   ABU25554 standard; protein; 365 AA.
DE   Protein encoded by Prokaryotic essential gene #11081.
PN   WO200271183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
  Query Match
  Best Local Similarity   21.2%;   Score 79.5;   DB 6;   Length 365;
RESULT 721
ID   AARS8703 standard; protein; 406 AA.
DE   HCMV IE-exon-4 subunit.
PN   WO9417810-A1.
PD   18-AUG-1994.
PA   (WIST-) WISTAR INST ANATOMY & BIOLOGY.
  Best Local Similarity   20.0%;   Score 79.5;   DB 2;   Length 406;
RESULT 722
ID   AAW27275 standard; protein; 406 AA.
DE   Human cytomegalovirus immediate-early exon 4 product.
PN   WO9740165-A1.
PD   30-OCT-1997.
PA   (WIST-) WISTAR INST ANATOMY & BIOLOGY.
  Query Match
  Best Local Similarity   19.3%;   Score 79.5;   DB 2;   Length 406;
RESULT 723
ID   ABB58483 standard; protein; 638 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 2241.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.

  Query Match
  Best Local Similarity   20.5%;   Score 79.5;   DB 4;   Length 638;
RESULT 724
ID   AAE13277 standard; protein; 723 AA.
DE   Human transporters and ion channels (TRICH)-4.
PN   WO200177174-A2.
PD   18-OCT-2001.
PA   (INCY-) INCYTE GENOMICS INC.
  Best Local Similarity   18.0%;   Score 79.5;   DB 5;   Length 723;
RESULT 725
ID   ADL12774 standard; protein; 723 AA.
DE   Human steroid-induced C3A liver cell protein #80.
PN   US6673549-B1.
PD   06-JAN-2004.
PA   (INCY-) INCYTE CORP.
  Query Match
  Best Local Similarity   18.0%;   Score 79.5;   DB 8;   Length 723;
RESULT 726
ID   AAW20696 standard; protein; 121 AA.
DE   H. Pylori secreted or periplasmic protein 05ae20220orf50.
PN   WO9640893-A1.
PD   19-DEC-1996.
PA   (ASTR) ASTRA AB.
  Query Match
  Best Local Similarity   21.4%;   Score 79;   DB 2;   Length 121;
RESULT 727
ID   ABB60462 standard; protein; 323 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 8178.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
  Query Match
  Best Local Similarity   18.8%;   Score 79;   DB 4;   Length 323;
RESULT 728
ID   AEB41478 standard; protein; 356 AA.
DE   L. pneumophila protein SEQ ID NO 5810.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP) INST PASTEUR.
PA   (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA   (CNRS) CNRS CENT NAT RECH SCI.
  Query Match
  Best Local Similarity   23.0%;   Score 79;   DB 9;   Length 356;
RESULT 729
ID   AEB38189 standard; protein; 358 AA.
DE   L. pneumophila protein SEQ ID NO 2521.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP) INST PASTEUR.
PA   (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA   (CNRS) CNRS CENT NAT RECH SCI.
  Query Match
  Best Local Similarity   23.0%;   Score 79;   DB 7;   Length 358;
RESULT 730
ID   ABR58610 standard; protein; 1531 AA.
DE   Human cancer related protein SEQ ID NO:267.
PN   WO200305138-A2.
PD   27-MAR-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
  Query Match
  Best Local Similarity   24.3%;   Score 79;   DB 6;   Length 1531;
RESULT 731
ID   ADB31753 standard; protein; 1531 AA.
DE   Human 59590 protein #SEQ ID 110.
PN   WO2003065984-A2.
PD   14-AUG-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
  Query Match
  Best Local Similarity   24.3%;   Score 79;   DB 7;   Length 1531;
RESULT 732

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ID   AEF11993 standard; protein; 1531 AA.
DE   Human heart alpha-kinase protein SEQ ID NO 2.
PN   WO200512435 9-A2.
PD   29-DEC-2005.
PA   (META-) METABOLEX INC.
           Query Match    6.6%;  Score 79;  DB 10;  Length 1531;
Best Local Similarity   24.3%;  Pred. No. 43;

RESULT 733
ID   AEF11995 standard; protein; 1536 AA.
DE   Human heart alpha-kinase Metabolex variant protein SEQ ID NO 4.
PN   WO200512435 9-A2.
PD   29-DEC-2005.
PA   (META-) METABOLEX INC.
           Query Match    6.6%;  Score 79;  DB 10;  Length 1536;
Best Local Similarity   24.3%;  Pred. No. 43;

RESULT 734
ID   ABU62069 standard; protein; 1597 AA.
DE   Human heart alpha-kinase (HK).
PN   US200217720 5-A1.
PD   28-NOV-2002.
PA   (RYAZ/) RYAZANOV A.
           Query Match    6.6%;  Score 79;  DB 6;  Length 1597;
Best Local Similarity   24.3%;  Pred. No. 45;

RESULT 735
ID   ABU62070 standard; protein; 1597 AA.
DE   Mouse heart alpha-kinase (HK).
PN   US200217720 5-A1.
PD   28-NOV-2002.
PA   (RYAZ/) RYAZANOV A.
           Query Match    6.6%;  Score 79;  DB 6;  Length 1597;
Best Local Similarity   24.3%;  Pred. No. 45;

RESULT 736
ID   ABO55689 standard; protein; 135 AA.
DE   Human genome derived single exon protein #1923.
PN   US200319470 4-A1.
PD   16-OCT-2003.
PA   (PENN/) PENN S G.
PA   (RANK/) RANK D R.
PA   (HANZ/) HANZEL D K.
           Query Match    6.6%;  Score 78.5;  DB 8;  Length 135;
Best Local Similarity   59.4%;  Pred. No. 1.7;

RESULT 737
ID   ADU02890 standard; protein; 165 AA.
DE   Novel human polypeptide seqid 1357.
PN   WO200409380 4-A2.
PD   04-NOV-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
           Query Match    6.6%;  Score 78.5;  DB 8;  Length 165;
Best Local Similarity   24.6%;  Pred. No. 2.2;

RESULT 738
ID   AEB38367 standard; protein; 205 AA.
DE   L. pneumophila protein SEQ ID NO 2699.
PN   WO200504964 2-A2.
PD   02-JUN-2005.
PA   (INSP) INST PASTEUR.
PA   (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA   (CNRS) CNRS CENT NAT RECH SCI.
           Query Match    6.6%;  Score 78.5;  DB 9;  Length 205;
Best Local Similarity   18.3%;  Pred. No. 3;

RESULT 739
ID   ADB10816 standard; protein; 228 AA.
DE   Alloiococcus otitis antigenic protein SEQ ID NO:4244.
PN   WO200304830 4-A2.
PD   12-JUN-2003.
PA   (AMHP ) WYETH HOLDINGS CORP.
           Query Match    6.6%;  Score 78.5;  DB 6;  Length 228;
Best Local Similarity   22.5%;  Pred. No. 3.5;

RESULT 740
ID   ABU36298 standard; protein; 239 AA.
DE   Protein encoded by Prokaryotic essential gene #21825.
PN   WO200277183 -A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Best Local Similarity   23.4%;  Query Match    6.6%;  Score 78.5;  DB 6;  Length 239;
                                 Pred. No. 3.7;

RESULT 741
ID   AD27174 standard; protein; 626 AA.
DE   Human TRICH-6, SEQ ID 6.
PN   WO200401329 3-A2.
PD   12-FEB-2004.
PA   (INCY-) INCYTE CORP.
           Query Match    6.6%;  Score 78.5;  DB 8;  Length 626;
Best Local Similarity   18.0%;  Pred. No. 14;

RESULT 742
ID   ABM84879 standard; protein; 648 AA.
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:5128.
PN   WO200402397 3-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
           Query Match    6.6%;  Score 78.5;  DB 8;  Length 648;
Best Local Similarity   18.0%;  Pred. No. 15;

RESULT 743
ID   ABM84877 standard; protein; 668 AA.
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:5126.
PN   WO200402397 3-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
           Query Match    6.6%;  Score 78.5;  DB 8;  Length 668;
Best Local Similarity   18.0%;  Pred. No. 15;

RESULT 744
ID   ABP29904 standard; protein; 669 AA.
DE   Streptococcus polypeptide SEQ ID NO 8984.
PN   WO200234771 -A2.
PD   02-MAY-2002.
PA   (GENO-) INST GENOMIC RES.
PA   (CHIR-) CHIRON SPA.
           Query Match    6.6%;  Score 78.5;  DB 5;  Length 669;
Best Local Similarity   23.5%;  Pred. No. 15;

RESULT 745
ID   ABP28724 standard; protein; 669 AA.
DE   Streptococcus polypeptide SEQ ID NO 6624.
PN   WO200234771 -A2.
PD   02-MAY-2002.
PA   (GENO-) INST GENOMIC RES.
PA   (CHIR-) CHIRON SPA.
           Query Match    6.6%;  Score 78.5;  DB 5;  Length 669;
Best Local Similarity   23.5%;  Pred. No. 15;

RESULT 746
ID   ADI21047 standard; protein; 703 AA.
DE   Novel human protein #22.
PN   WO200302514 8-A2.
PD   27-MAR-2003.
PA   (HYSE-) HYSEQ INC.
           Query Match    6.6%;  Score 78.5;  DB 7;  Length 703;
Best Local Similarity   18.0%;  Pred. No. 17;

RESULT 747
ID   ABM84882 standard; protein; 711 AA.
DE   Human diagnostic and therapeutic SEQ ID NO:5131.
PN   WO200402397 3-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
           Query Match    6.6%;  Score 78.5;  DB 8;  Length 711;
Best Local Similarity   18.0%;  Pred. No. 17;

RESULT 748
ID   ABP52105 standard; protein; 723 AA.
DE   Homo sapiens ABC transporter ABCB9 protein SEQ ID NO:57.
PN   EP121706 6-A1.
PD   26-JUN-2002.
PA   (UYGE-) UNIV GENT.
           Query Match    6.6%;  Score 78.5;  DB 5;  Length 723;
Best Local Similarity   18.0%;  Pred. No. 17;

RESULT 749
ID   ADQ97094 standard; protein; 723 AA.
DE   Human cancer associated sequence HP1-10-005, SEQ ID 70.
PN   WO200406030 4-A2.
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PD   22-JUL-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
Query Match   6.6%; Score 78.5; DB 8; Length 723;
Best Local Similarity 18.0%; Pred. No. 17;
RESULT 750
ID   AAB02437 standard; protein; 766 AA.
DE   Human ATP binding cassette, ABCB9 transporter protein.
PN   WO200140305-A1.
PD   07-JUN-2001.
PA   (ACTI-) ACTIVE PASS PHARM INC.
Query Match   6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 19;
RESULT 751
ID   AAB02441 standard; protein; 766 AA.
DE   Human ATP binding cassette, ABCB9 transporter protein mutant K545R.
PN   WO200140305-A1.
PD   07-JUN-2001.
PA   (ACTI-) ACTIVE PASS PHARM INC.
Query Match   6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 19;
RESULT 752
ID   AAB02442 standard; protein; 766 AA.
DE   Human ATP binding cassette, ABCB9 transporter protein mutant D667N.
PN   WO200140305-A1.
PD   07-JUN-2001.
PA   (ACTI-) ACTIVE PASS PHARM INC.
Query Match   6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 19;
RESULT 753
ID   AAG67163 standard; protein; 766 AA.
DE   Amino acid sequence of a human 33894 transporter polypeptide.
PN   WO200164875-A2.
PD   07-SEP-2001.
PA   (MILL-) MILLENNIUM PHARM INC.
Query Match   6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 19;
RESULT 754
ID   AAG79246 standard; protein; 766 AA.
DE   Amino acid sequence of a human TAP-like (HUTAPL) polypeptide.
PN   WO200173018-A2.
PD   04-OCT-2001.
PA   (MERE) MERCK PATENT GMBH.
Query Match   6.6%; Score 78.5; DB 4; Length 766;
Best Local Similarity 18.0%; Pred. No. 19;
RESULT 755
ID   ABB98345 standard; protein; 766 AA.
DE   Human ABC transporter ABCB9 SEQ ID NO 6.
PN   WO200264781-A2.
PD   22-AUG-2002.
PA   (ACTI-) ACTIVE PASS PHARM INC.
Query Match   6.6%; Score 78.5; DB 5; Length 766;
Best Local Similarity 18.0%; Pred. No. 19;
RESULT 756
ID   AAE21170 standard; protein; 766 AA.
DE   Human TRICH-14 protein.
PN   WO200212340-A2.
PD   14-FEB-2002.
PA   (INCY-) INCYTE GENOMICS INC.
Query Match   6.6%; Score 78.5; DB 5; Length 766;
Best Local Similarity 18.0%; Pred. No. 19;
RESULT 757
ID   ADQ97096 standard; protein; 766 AA.
DE   Human cancer associated sequence HP2-10-005, SEQ ID 72.
PN   WO200406030-A2.
PD   22-JUL-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
Query Match   6.6%; Score 78.5; DB 8; Length 766;
Best Local Similarity 18.0%; Pred. No. 19;
RESULT 758
ID   AAG20805 standard; protein; 377 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 23131.
PN   EP1033405-A2.
PD   06-SEP-2000.

Query Match   6.5%; Score 78; DB 3; Length 377;
Best Local Similarity 23.8%; Pred. No. 8;
RESULT 759
ID   AAG20804 standard; protein; 442 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 23130.
PN   EP1033405-A2.
PD   06-SEP-2000.
Query Match   6.5%; Score 78; DB 3; Length 442;
Best Local Similarity 23.8%; Pred. No. 10;
RESULT 760
ID   AAU35445 standard; protein; 471 AA.
DE   Haemophilus influenzae cellular proliferation protein #186.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   6.5%; Score 78; DB 4; Length 471;
Best Local Similarity 25.0%; Pred. No. 11;
RESULT 761
ID   ABU30411 standard; protein; 471 AA.
DE   Protein encoded by Prokaryotic essential gene #15938.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   6.5%; Score 78; DB 6; Length 471;
Best Local Similarity 25.0%; Pred. No. 11;
RESULT 762
ID   AAG20803 standard; protein; 489 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 23129.
PN   EP1033405-A2.
PD   06-SEP-2000.
Query Match   6.5%; Score 78; DB 3; Length 489;
Best Local Similarity 23.8%; Pred. No. 11;
RESULT 763
ID   ABG17374 standard; protein; 280 AA.
DE   Novel human diagnostic protein #17365.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (INSP) INST PASTEUR.
Query Match   6.5%; Score 77.5; DB 5; Length 269;
Best Local Similarity 22.0%; Pred. No. 5.7;
RESULT 764
ID   ABB49039 standard; protein; 269 AA.
DE   Listeria monocytogenes protein #1743.
PN   WO200177335-A2.
PD   18-OCT-2001.
Query Match   6.5%; Score 77.5; DB 4; Length 280;
Best Local Similarity 21.9%; Pred. No. 6.1;
RESULT 765
ID   ABO00771 standard; protein; 280 AA.
DE   Polypeptide encoded by novel human contig #22.
PN   WO200303013-A2.
PD   20-MAR-2003.
PA   (HYSE-) HYSEQ INC.
Query Match   6.5%; Score 77.5; DB 6; Length 280;
Best Local Similarity 21.9%; Pred. No. 6.1;
RESULT 766
ID   ABU48889 standard; protein; 327 AA.
DE   Protein encoded by Prokaryotic essential gene #34416.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   6.5%; Score 77.5; DB 6; Length 327;
Best Local Similarity 24.8%; Pred. No. 7.5;
RESULT 767
ID   AAW13576 standard; protein; 438 AA.
DE   Mouse Batten disease polypeptide CLN3 homologue.
PN   WO9708308-A1.
PD   06-MAR-1997.
PA   (GEHO) GEN HOSPITAL CORP.
     (UYLE-) RIJKSUNIV LEIDEN.
Query Match   6.5%; Score 77.5; DB 2; Length 438;
Best Local Similarity 27.6%; Pred. No. 11;

RESULT 768
ID   ADS42965 standard; protein; 491 AA.
DE   Bacterial polypeptide #21395.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match   22.6%;
     Best Local Similarity   6.5%;   Score 77.5;   DB 8;   Pred. No. 13;   Length 491;

RESULT 769
ID   ADC42919 standard; protein; 892 AA.
DE   Variola smallpox virus A10L.
PN   WO2003017943-A2.
PD   06-MAR-2003.
PA   (MYRI-) MYRIAD GENETICS INC.
     Query Match   22.7%;
     Best Local Similarity   6.5%;   Score 77.5;   DB 7;   Pred. No. 30;   Length 892;

RESULT 770
ID   AEF63571 standard; protein; 930 AA.
DE   Ostreococcus tauri phospholipase 2 protein.
PN   WO2006008099-A2.
PD   26-JAN-2006.
PA   (BADI) BASF PLANT SCI GMBH.
     Query Match   19.7%;
     Best Local Similarity   6.5%;   Score 77.5;   DB 10;   Pred. No. 32;   Length 930;

RESULT 771
ID   AAR88413 standard; protein; 353 AA.
DE   High-affinity melatonin-1a receptor.
PN   WO9535320-A1.
PD   28-DEC-1995.
PA   (MASS-) MASSACHUSETTS GEN HOSPITAL.
     Query Match   22.1%;
     Best Local Similarity   6.4%;   Score 77;   DB 2;   Pred. No. 9.6;   Length 353;

RESULT 772
ID   AAW23958 standard; protein; 353 AA.
DE   Mouse melatonin 1a receptor.
PN   WO9803549-A1.
PD   29-JAN-1998.
PA   (GEHO) GEN HOSPITAL CORP.
     Query Match   22.1%;
     Best Local Similarity   6.4%;   Score 77;   DB 2;   Pred. No. 9.6;   Length 353;

RESULT 773
ID   ABB07571 standard; protein; 353 AA.
DE   Mouse melatonin 1a (Mella) receptor.
PN   US6326526-B1.
PD   04-DEC-2001.
PA   (BRIM) BRISTOL-MYERS SQUIBB CO.
     Query Match   22.1%;
     Best Local Similarity   6.4%;   Score 77;   DB 5;   Pred. No. 9.6;   Length 353;

RESULT 774
ID   ADO29553 standard; protein; 353 AA.
DE   Mouse GPCR MTNR1A, SEQ ID NO:655.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
PA   (GEHO) GEN HOSPITAL CORP.
     Query Match   22.1%;
     Best Local Similarity   6.4%;   Score 77;   DB 8;   Pred. No. 9.6;   Length 353;

RESULT 775
ID   ADM25403 standard; protein; 383 AA.
DE   Hyperthermophile Methanopyrus kandleri protein #9.
PN   WO2003076575-A2.
PD   18-SEP-2003.
PA   (MALY/) MALYKH A.
PA   (FIDE-) FIDELITY SYSTEMS INC.
     Query Match   24.8%;
     Best Local Similarity   6.4%;   Score 77;   DB 7;   Pred. No. 11;   Length 383;

RESULT 776
ID   ADQ95948 standard; protein; 490 AA.
DE   T cell activation associated protein #63.

RESULT 777
ID   ADQ96002 standard; protein; 490 AA.
DE   T cell activation associated protein #90.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
     Query Match   19.5%;
     Best Local Similarity   6.4%;   Score 77;   DB 8;   Pred. No. 15;   Length 490;

RESULT 778
ID   AAG42521 standard; protein; 648 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 53040.
PN   EP1033405-A2.
PD   06-SEP-2000.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   19.5%;
     Best Local Similarity   6.4%;   Score 77;   DB 3;   Pred. No. 15;   Length 648;

RESULT 779
ID   ABU16172 standard; protein; 650 AA.
DE   Protein encoded by Prokaryotic essential gene #1699.
PN   WO2002077183-A2.
PD   03-OCT-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match   27.5%;
     Best Local Similarity   6.4%;   Score 77;   DB 6;   Pred. No. 22;   Length 650;

RESULT 780
ID   ABM72713 standard; protein; 650 AA.
DE   Staphylococcus aureus protein #1953.
PN   WO2002094868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match   27.5%;
     Best Local Similarity   6.4%;   Score 77;   DB 6;   Pred. No. 22;   Length 650;

RESULT 781
ID   AAG42519 standard; protein; 728 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 53039.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   20.4%;
     Best Local Similarity   6.4%;   Score 77;   DB 3;   Pred. No. 24;   Length 728;

RESULT 782
ID   AAG42520 standard; protein; 690 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 53038.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   20.4%;
     Best Local Similarity   6.4%;   Score 77;   DB 3;   Pred. No. 26;   Length 690;

RESULT 783
ID   AAG32549 standard; protein; 805 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 39287.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   20.4%;
     Best Local Similarity   6.4%;   Score 77;   DB 3;   Pred. No. 30;   Length 805;

RESULT 784
ID   AAG32548 standard; protein; 847 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 39286.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   20.4%;
     Best Local Similarity   6.4%;   Score 77;   DB 3;   Pred. No. 32;   Length 847;

RESULT 785
ID   AAG32547 standard; protein; 991 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 39285.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   20.4%;
     Best Local Similarity   6.4%;   Score 77;   DB 3;   Pred. No. 40;   Length 991;

RESULT 786
ID   ABP52133 standard; protein; 1025 AA.

DE Plasmodium falciparummultidrug resistance protein SEQ ID NO:85.
PN EP1217066-A1.
PD 26-JUN-2002.
PA (UYGE-) UNIV GENT.
Query Match 6.4%; Score 77; DB 5; Length 1025;
Best Local Similarity 20.6%; Pred. No. 42;

RESULT 787
ID AAG42381 standard; protein; 1047 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52849.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 1047;
Best Local Similarity 20.4%; Pred. No. 43;

RESULT 788
ID AAG42380 standard; protein; 1191 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52848.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 1191;
Best Local Similarity 20.4%; Pred. No. 52;

RESULT 789
ID AAG42379 standard; protein; 1202 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52847.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 1202;
Best Local Similarity 20.4%; Pred. No. 52;

RESULT 790
ID AAR29527 standard; protein; 2510 AA.
DE HCV antigen T7N1-30.
PN EP518313-A2.
PD 16-DEC-1992.
PA (MITU) MITSUBISHI KASEI CORP.
Query Match 6.4%; Score 77; DB 2; Length 2510;
Best Local Similarity 22.5%; Pred. No. 1.5e+02;

RESULT 791
ID ADX40818 standard; protein; 3010 AA.
DE HCV polymerase protein #41.
PN WO2005012502-A2.
PD 10-FEB-2005.
PA (EPIM-) EPIMMUNE INC.
Query Match 6.4%; Score 77; DB 9; Length 3010;
Best Local Similarity 22.5%; Pred. No. 1.9e+02;

RESULT 792
ID ADX40816 standard; protein; 3010 AA.
DE HCV polymerase protein #39.
PN WO2005012502-A2.
PD 10-FEB-2005.
PA (EPIM-) EPIMMUNE INC.
Query Match 6.4%; Score 77; DB 9; Length 3010;
Best Local Similarity 22.5%; Pred. No. 1.9e+02;

RESULT 793
ID ADT56855 standard; protein; 195 AA.
DE Plant polypeptide, SEQ ID 6932.
PN US2004216190-A1.
PD 28-OCT-2004.
PA (KOVA/) KOVALIC D K.
Query Match 6.4%; Score 76.5; DB 8; Length 195;
Best Local Similarity 25.8%; Pred. No. 4.8;

RESULT 794
ID ADF74966 standard; protein; 249 AA.
DE Human 164-1h protein (SeqID 25).
PN WO2003097686-A1.
PD 27-NOV-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.4%; Score 76.5; DB 8; Length 249;
Best Local Similarity 23.3%; Pred. No. 6.7;

RESULT 795
ID ADC01137 standard; protein; 278 AA.
DE Enterohaemorragic E. coli 0157:H7-specific protein SEQ ID NO: 1181.
PN JP2002355074-A.
PD 10-DEC-2002.
PA (UYTS-) UNIV TSUKUBA.
Query Match 6.4%; Score 76.5; DB 7; Length 278;
Best Local Similarity 28.5%; Pred. No. 7.9;

RESULT 796
ID AE065827 standard; protein; 435 AA.
DE Klebsiella pneumoniae polypeptide seqid 12344.
PN US6610336-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.4%; Score 76.5; DB 7; Length 435;
Best Local Similarity 21.8%; Pred. No. 15;

RESULT 797
ID ADF74969 standard; protein; 481 AA.
DE Human 164-1b protein (SeqID 28).
PN WO2003097686-A1.
PD 27-NOV-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.4%; Score 76.5; DB 8; Length 481;
Best Local Similarity 23.3%; Pred. No. 17;

RESULT 798
ID AAR90765 standard; protein; 494 AA.
DE Human K+ channel 2 mature protein.
PN WO9603415-A1.
PD 08-FEB-1996.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%; Score 76.5; DB 2; Length 494;
Best Local Similarity 21.3%; Pred. No. 17;

RESULT 799
ID AAW42996 standard; protein; 494 AA.
DE Putative mature potassium channel 2 protein.
PN US5710019-A.
PD 20-JAN-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%; Score 76.5; DB 2; Length 494;
Best Local Similarity 21.3%; Pred. No. 17;

RESULT 800
ID ABP58356 standard; protein; 494 AA.
DE Human potassium channel subunit Kv5.1.
PN WO200296944-A2.
PD 05-DEC-2002.
PA (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
Query Match 6.4%; Score 76.5; DB 6; Length 494;
Best Local Similarity 21.3%; Pred. No. 17;

RESULT 801
ID ADC99155 standard; protein; 494 AA.
DE Human mature K+ channel 2 protein.
PN US2003092895-A1.
PD 15-MAY-2003.
PA (LIYY/) LI Y.
PA (ADAM/) ADAMS M D.
PA (WHIT/) WHITE O R.
Query Match 6.4%; Score 76.5; DB 7; Length 494;
Best Local Similarity 21.3%; Pred. No. 17;

RESULT 802
ID AAW20085 standard; protein; 509 AA.
DE Human hypothetical protein FLJ20371-encoding cDNA.
PN WO2004061123-A2.
PD 22-JUL-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 6.4%; Score 76.5; DB 2; Length 509;
Best Local Similarity 19.2%; Pred. No. 18;

RESULT 803
ID ADQ07984 standard; protein; 526 AA.
DE Helicobacter pylori cytoplasmic protein, 10009666.aa.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 6.4%; Score 76.5; DB 8; Length 526;
Best Local Similarity 21.3%; Pred. No. 19;

RESULT 804
ID ADP25065 standard; protein; 526 AA.
DE PRO polypeptide SEQ ID NO:2243.
PN WO2004041170-A2.
PD 21-MAY-2004.
Query Match 6.4%; Score 76.5; DB 8; Length 526;
Best Local Similarity 15.7%; Pred. No. 19;

PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 76.5; DB 8; Length 526;
Best Local Similarity 15.7%; Pred. No. 19;
RESULT 805
ID ADU06638 standard; protein; 526 AA.
DE Novel bronchial cancer-associated human protein SeqID864.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 6.4%; Score 76.5; DB 8; Length 526;
Best Local Similarity 15.7%; Pred. No. 19;
RESULT 806
ID ADB63857 standard; protein; 555 AA.
DE Human protein encoded by clone ASTRO20053430.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.4%; Score 76.5; DB 7; Length 555;
Best Local Similarity 23.3%; Pred. No. 21;
RESULT 807
ID ABB08159 standard; protein; 570 AA.
DE Human cytoskeleton-associated protein (CSAP)-3 (ID: 7091536CD1).
PN WO200242330-A2.
PD 30-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.4%; Score 76.5; DB 5; Length 570;
Best Local Similarity 23.3%; Pred. No. 21;
RESULT 808
ID AAW20918 standard; protein; 593 AA.
DE H. pylori transporter protein, 14gp12o15orf14.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 6.4%; Score 76.5; DB 2; Length 593;
Best Local Similarity 19.2%; Pred. No. 22;
RESULT 809
ID ADN46225 standard; protein; 615 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID103.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 6.4%; Score 76.5; DB 8; Length 615;
Best Local Similarity 22.6%; Pred. No. 24;
RESULT 810
ID ADN21126 standard; protein; 2539 AA.
DE Bacterial polypeptide #3779.
PN US20032336 75-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.4%; Score 76.5; DB 8; Length 2539;
Best Local Similarity 22.1%; Pred. No. 1.7e+02;
RESULT 811
ID ADH88107 standard; protein; 195 AA.
DE Enterococcus faecalis polypeptide #2587.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.4%; Score 76; DB 7; Length 195;
Best Local Similarity 25.9%; Pred. No. 5.5;
RESULT 812
ID AAG09592 standard; protein; 274 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7586.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 76; DB 3; Length 274;

Best Local Similarity 26.7%; Pred. No. 8.8;
RESULT 813
ID AAG09591 standard; protein; 287 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7585.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 76; DB 3; Length 287;
Best Local Similarity 26.7%; Pred. No. 9.4;
RESULT 814
ID ADQ96244 standard; protein; 366 AA.
DE T cell activation associated protein #211.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAHI-) ASAHI KASEI PHARMA CORP.
Query Match 6.4%; Score 76; DB 8; Length 366;
Best Local Similarity 22.0%; Pred. No. 13;
RESULT 815
ID ADQ96246 standard; protein; 366 AA.
DE T cell activation associated protein #212.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAHI-) ASAHI KASEI PHARMA CORP.
Query Match 6.4%; Score 76; DB 8; Length 366;
Best Local Similarity 22.0%; Pred. No. 18;
RESULT 816
ID ABB89424 standard; protein; 456 AA.
DE Human colon cancer antigen protein sequence SEQ ID NO:940.
PN WO200190104-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%; Score 76; DB 5; Length 456;
Best Local Similarity 22.0%; Pred. No. 24;
RESULT 817
ID AAB53400 standard; protein; 557 AA.
DE Human polypeptide SEQ ID NO 1800.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%; Score 76; DB 3; Length 557;
Best Local Similarity 22.0%; Pred. No. 24;
RESULT 818
ID AAY44945 standard; protein; 593 AA.
DE Wheat sulphate permease-2.
PN WO2000004154-A2.
PD 27-JAN-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 6.4%; Score 76; DB 3; Length 593;
Best Local Similarity 22.0%; Pred. No. 26;
RESULT 819
ID ADN22849 standard; protein; 1402 AA.
DE Bacterial polypeptide #5502.
PN US20032336 75-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.4%; Score 76; DB 8; Length 1402;
Best Local Similarity 20.2%; Pred. No. 85;
RESULT 820
ID AEF10990 standard; protein; 1783 AA.
DE C. elegans VDCC alpha 1 subunit, Cav2.1.
PN US20052 88489-A1.
PD 29-DEC-2005.
PA (HIRS/) HIRSCH J A.
Query Match 6.4%; Score 76; DB 10; Length 1783;
Best Local Similarity 18.5%; Pred. No. 1.2e+02;
RESULT 821
ID ADN23383 standard; protein; 1917 AA.
DE Bacterial polypeptide #6036.
PN US20032336 75-A1.
PD 18-DEC-2003.

Left column

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PA  (CAOY/) CAO Y.
PA  (HINK/) HINKLE G J.
PA  (SLAT/) SLATER S C.
PA  (CHEN/) CHEN X.
PA  (GOLD/) GOLDMAN B S.
    Query Match   Best Local Similarity  18.5%;
    6.3%;  Score 76;  DB 8;  Pred. No. 1.3e+02;  Length 1917;

RESULT 823
ID  ADX40794 standard; protein; 3010 AA.
DE  HCV polymerase protein #17.
PN  WO2005012502-A2.
PD  10-FEB-2005.
PA  (EPIM-) EPIMMUNE INC.
    Query Match   Best Local Similarity  25.4%;
    6.4%;  Score 76;  DB 9;  Pred. No. 2.5e+02;  Length 3010;

RESULT 824
ID  ADX40791 standard; protein; 3010 AA.
DE  HCV polymerase protein #14.
PN  WO2005012502-A2.
PD  10-FEB-2005.
PA  (EPIM-) EPIMMUNE INC.
    Query Match   Best Local Similarity  25.4%;
    6.4%;  Score 76;  DB 9;  Pred. No. 2.5e+02;  Length 3010;

RESULT 825
ID  ADX40792 standard; protein; 3010 AA.
DE  HCV polymerase protein #15.
PN  WO2005012502-A2.
PD  10-FEB-2005.
PA  (EPIM-) EPIMMUNE INC.
    Query Match   Best Local Similarity  26.9%;
    6.4%;  Score 76;  DB 9;  Pred. No. 2.5e+02;  Length 3010;

RESULT 826
ID  ABB63150 standard; protein; 228 AA.
DE  Drosophila melanogaster polypeptide SEQ ID No 16242.
PN  US6697703-B1.
PD  02-MAR-2004.
PA  (PEKE ) PE CORP NY.
    Query Match   Best Local Similarity  21.8%;
    6.3%;  Score 76;  DB 4;  Pred. No. 7.8;  Length 228;

RESULT 827
ID  ADK46633 standard; protein; 263 AA.
DE  Streptococcus pneumoniae protein, Seq ID No 3148.
PN  US6689693-B1.
PD  27-SEP-2001.
PA  (GENO-) GENOME THERAPEUTICS CORP.
    Query Match   Best Local Similarity  18.0%;
    6.3%;  Score 75.5;  DB 8;  Pred. No. 9.5;  Length 263;

RESULT 828
ID  ADM92206 standard; protein; 263 AA.
DE  S pneumoniae antigenic protein sequence SeqID403.
PN  WO200402069-A2.
PD  11-MAR-2004.
PA  (MICR-) MICROBIAL TECHNICS LTD.
    Query Match   Best Local Similarity  18.0%;
    6.3%;  Score 75.5;  DB 9;  Pred. No. 9.5;  Length 263;

RESULT 829
ID  ADR96242 standard; protein; 264 AA.
DE  Novel S. pneumoniae protein sequence, SEQ ID 4877.
PN  US6800744-B1.
PD  05-OCT-2004.
PA  (GENO-) GENOME THERAPEUTICS CORP.
    Query Match   Best Local Similarity  18.0%;
    6.3%;  Score 75.5;  DB 3;  Pred. No. 9.6;  Length 264;

RESULT 830
ID  AEA60112 standard; protein; 264 AA.
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Right column

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DE  Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:4877.
PN  US2005136404-A1.
PD  23-JUN-2005.
PA  (BUSH/) BUSH D.
PA  (DOUC/) DOUCETTE-STAMM L A.
    Query Match   Best Local Similarity  18.0%;
    6.3%;  Score 75.5;  DB 9;  Pred. No. 9.6;  Length 264;

RESULT 831
ID  ABU02182 standard; protein; 276 AA.
DE  S. pneumoniae type 4 strain protein from coding region #1759.
PN  WO200277021-A2.
PD  03-OCT-2002.
PA  (CHIR-) CHIRON SPA.
PA  (GENO-) INST GENOMIC RES.
    Query Match   Best Local Similarity  18.0%;
    6.3%;  Score 75.5;  DB 6;  Pred. No. 10;  Length 276;

RESULT 832
ID  ABG93285 standard; protein; 342 AA.
DE  C. albicans BAX-associated protein fragment SEQ ID 528.
PN  WO200264766-A2.
PD  22-AUG-2002.
PA  (JANC ) JANSSEN PHARM NV.
    Query Match   Best Local Similarity  21.9%;
    6.3%;  Score 75.5;  DB 5;  Pred. No. 14;  Length 342;

RESULT 833
ID  AAB15936 standard; protein; 352 AA.
DE  E. coli proliferation associated protein sequence SEQ ID NO:293.
PN  WO200044906-A2.
PD  03-AUG-2000.
PA  (ELIT-) ELITRA PHARM INC.
    Query Match   Best Local Similarity  31.7%;
    6.3%;  Score 75.5;  DB 3;  Pred. No. 14;  Length 352;

RESULT 834
ID  ADH51470 standard; protein; 363 AA.
DE  Rat MT1 receptor amino acid sequence #SEQ ID 2.
PN  FR2835847-A1.
PD  15-AUG-2003.
PA  (SERV-) LES LAB SERVIER SA.
    Query Match   Best Local Similarity  23.5%;
    6.3%;  Score 75.5;  DB 7;  Pred. No. 15;  Length 363;

RESULT 835
ID  AAU03851 standard; protein; 397 AA.
DE  G protein-coupled receptor-like (GPCR-like) receptor protein #23.
PN  WO200138533-A2.
PD  31-MAY-2001.
PA  (PHAA ) PHARMACIA & UPJOHN.
    Query Match   Best Local Similarity  19.1%;
    6.3%;  Score 75.5;  DB 4;  Pred. No. 17;  Length 397;

RESULT 836
ID  ADU92092 standard; protein; 415 AA.
DE  Escherichia coli TnaB protein.
PN  EP1484410-A1.
PD  08-DEC-2004.
PA  (AJIN ) AJINOMOTO KK.
    Query Match   Best Local Similarity  19.1%;
    6.3%;  Score 75.5;  DB 4;  Pred. No. 17;  Length 415;

RESULT 837
ID  ABB41698 standard; protein; 430 AA.
DE  L. pneumophila protein SEQ ID NO 6030.
PN  WO2005049642-A2.
PD  02-JUN-2005.
PA  (INSP ) INST PASTEUR.
PA  (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA  (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA  (CNRS ) CNRS CENT NAT RECH SCI.
    Query Match   Best Local Similarity  20.5%;
    6.3%;  Score 75.5;  DB 9;  Pred. No. 18;  Length 430;

RESULT 838
ID  AAU03852 standard; protein; 433 AA.
DE  G protein-coupled receptor-like (GPCR-like) receptor protein #24.
PN  WO200138533-A2.
PD  31-MAY-2001.
PA  (PHAA ) PHARMACIA & UPJOHN.
    Query Match   Best Local Similarity  25.5%;
    6.3%;  Score 75.5;  DB 9;  Pred. No. 19;  Length 433;
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          Query Match              6.3%;
          Best Local Similarity   19.1%;   Score 75.5;   DB 4;   Length 433;

RESULT 839
ID   AEB38437 standard; protein; 436 AA.
DE   L. pneumophila protein SEQ ID NO 2769.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP ) INST PASTEUR.
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
          Query Match              6.3%;
          Best Local Similarity   25.5%;   Score 75.5;   DB 9;   Length 436;

RESULT 840
ID   ADS24439 standard; protein; 463 AA.
DE   Bacterial polypeptide #13272.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
          Query Match              6.3%;
          Best Local Similarity   21.4%;   Score 75.5;   DB 8;   Length 463;

RESULT 841
ID   ADO2907 standard; protein; 471 AA.
DE   Mouse GPCR HTR2A, SEQ ID NO:609.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
          Query Match              6.3%;
          Best Local Similarity   21.0%;   Score 75.5;   DB 8;   Length 471;

RESULT 842
ID   AAU03820 standard; protein; 499 AA.
DE   G protein-coupled receptor-like (GPCR-like) receptor protein #19.
PN   WO200138533-A2.
PD   31-MAY-2001.
PA   (PHA ) PHARMACIA & UPJOHN.
          Query Match              6.3%;
          Best Local Similarity   19.1%;   Score 75.5;   DB 4;   Length 499;

RESULT 843
ID   ADM72132 standard; protein; 392 AA.
DE   Human NTRAN polypeptide (clone ID 752455CD1).
PN   WO2004022705-A2.
PD   18-MAR-2004.
PA   (INCY-) INCYTE CORP.
          Query Match              6.3%;
          Best Local Similarity   21.0%;   Score 75;   DB 8;   Length 392;

RESULT 844
ID   ABM90212 standard; protein; 404 AA.
DE   Rice abiotic stress responsive polypeptide SEQ ID NO:8934.
PN   WO2003008540-A2.
PD   30-JAN-2003.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
          Query Match              6.3%;
          Best Local Similarity   15.6%;   Score 75;   DB 7;   Length 404;

RESULT 845
ID   AEB39222 standard; protein; 418 AA.
DE   L. pneumophila protein SEQ ID NO 3554.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP ) INST PASTEUR.
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
          Query Match              6.3%;
          Best Local Similarity   20.7%;   Score 75;   DB 9;   Length 418;

RESULT 846
ID   AEB35772 standard; protein; 437 AA.
DE   L. pneumophila protein SEQ ID NO 104.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP ) INST PASTEUR.
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
          Query Match              6.3%;
          Best Local Similarity   20.7%;   Score 75;   DB 9;   Length 437;

RESULT 847
ID   AAU45917 standard; protein; 445 AA.
DE   Propionibacterium acnes immunogenic protein #6813.
PN   WO200181581-A2.
PD   01-NOV-2001.
PA   (CORI-) CORIXA CORP.
          Query Match              6.3%;
          Best Local Similarity   24.8%;   Score 75;   DB 4;   Length 445;

RESULT 848
ID   ABM42436 standard; protein; 445 AA.
DE   Propionibacterium acnes predicted ORF-encoded polypeptide #7112.
PN   WO2003033515-A1.
PD   24-APR-2003.
PA   (CORI-) CORIXA CORP.
          Query Match              6.3%;
          Best Local Similarity   24.8%;   Score 75;   DB 6;   Length 445;

RESULT 849
ID   ABM87563 standard; protein; 452 AA.
DE   Rice abiotic stress responsive polypeptide SEQ ID NO:5809.
PN   WO2003008540-A2.
PD   30-JAN-2003.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
          Query Match              6.3%;
          Best Local Similarity   15.6%;   Score 75;   DB 7;   Length 452;

RESULT 850
ID   ADA34178 standard; protein; 467 AA.
DE   Acinetobacter baumannii protein #1339.
PN   US6562958-B1.
PD   13-MAY-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
          Query Match              6.3%;
          Best Local Similarity   23.1%;   Score 75;   DB 6;   Length 467;

RESULT 851
ID   ADR14597 standard; protein; 473 AA.
DE   Human NF-kappaB pathway-associated protein SeqID598.
PN   WO2004065577-A2.
PD   05-AUG-2004.
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
          Query Match              6.3%;
          Best Local Similarity   21.0%;   Score 75;   DB 8;   Length 473;

RESULT 852
ID   ADP99318 standard; protein; 480 AA.
DE   Human transporter and ion channel (TRICH) protein - SEQ ID 3.
PN   WO2004048599-A2.
PD   10-JUN-2004.
PA   (INCY-) INCYTE CORP.
          Query Match              6.3%;
          Best Local Similarity   21.0%;   Score 75;   DB 8;   Length 480;

RESULT 853
ID   ADH86490 standard; protein; 549 AA.
DE   Enterococcus faecalis polypeptide #970.
PN   US6617156-B1.
PD   09-SEP-2003.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.
          Query Match              6.3%;
          Best Local Similarity   18.7%;   Score 75;   DB 7;   Length 549;

RESULT 854
ID   ADX80121 standard; protein; 635 AA.
DE   Plant full length insert polypeptide seqid 49487.
PN   US2004034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S B.
PA   (TABA/) TABASKA J E.
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PA   (CAOY/) CAO Y.
Query Match   6.3%;   Score 75; DB 8; Length 635;
Best Local Similarity 25.3%; Pred. No. 37;

RESULT 855
ID   AAR54066 standard; protein; 1051 AA.
DE   Non-A, non-B hepatitis virus gene #4 product.
PN   JP06141870-A.
PD   24-MAY-1994.
PA   (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
PA   (SANW-) SANWA KAGAKU KENKYUSHO CO.
Query Match   6.3%;   Score 75; DB 2; Length 1051;
Best Local Similarity 23.4%; Pred. No. 75;

RESULT 856
ID   AAR98361 standard; protein; 1051 AA.
DE   5'UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#4).
PN   EP1308459-A2.
PN   JP07133291-A.
PD   07-MAY-2003.
PD   23-MAY-1995.
PA   (TOFU) TONEN CORP.
Query Match   6.3%;   Score 75; DB 2; Length 1051;
Best Local Similarity 23.4%; Pred. No. 75;

RESULT 857
ID   ADB64712 standard; protein; 1131 AA.
DE   Human protein encoded by clone NT2NE20077270.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
PA   (PEKE) PE CORP NY.
Query Match   6.3%;   Score 75; DB 7; Length 1131;
Best Local Similarity 23.9%; Pred. No. 83;

RESULT 858
ID   ABB64494 standard; protein; 2248 AA.
DE   Drosophila melanogaster rutabaga protein.
PN   WO200103704-A2.
PD   18-DEC-2003.
PA   (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match   6.3%;   Score 75; DB 4; Length 2248;
Best Local Similarity 23.9%; Pred. No. 2.1e+02;

RESULT 859
ID   ADG20763 standard; protein; 2248 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 20274.
PN   WO200103704-A2.
PD   18-DEC-2003.
PA   (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
Query Match   6.3%;   Score 75; DB 8; Length 2248;
Best Local Similarity 22.9%; Pred. No. 2.1e+02;

RESULT 860
ID   ADQ89656 standard; protein; 2248 AA.
DE   Antagonist of cell cycle progression polypeptide #43.
PN   WO2004063362-A2.
PD   29-JUL-2004.
PA   (CYCL-) CYCLACEL LTD.
Query Match   6.3%;   Score 75; DB 8; Length 2248;
Best Local Similarity 22.9%; Pred. No. 2.1e+02;

RESULT 861
ID   ADX40796 standard; protein; 3010 AA.
DE   HCV polymerase protein #19.
PN   WO2005012502-A2.
PD   10-FEB-2005.
PA   (EPIM-) EPIMMUNE INC.
Query Match   6.3%;   Score 75; DB 9; Length 3010;
Best Local Similarity 22.9%; Pred. No. 3.2e+02;

RESULT 862
ID   AAB66797 standard; protein; 200 AA.
DE   Porcine reproductive and respiratory syndrome virus ORF #5 protein.
PN   WO200102858-A1.
PD   11-JAN-2001.
PA   (MOLE-) INST MOLECULAR AGROBIOLOGY.
PA   (MATE-) INST MATERIALS RES & ENG.
Query Match   6.2%;   Score 74.5; DB 4; Length 200;
Best Local Similarity 25.4%; Pred. No. 8.6;

RESULT 863
ID   ADF74954 standard; protein; 256 AA.
DE   Rat 164-1h protein (SeqID 13).
PN   WO2003097686-A1.
PD   27-NOV-2003.
PA   (TAKE) TAKEDA CHEM IND LTD.
Query Match   6.2%;   Score 74.5; DB 8; Length 256;
Best Local Similarity 23.3%; Pred. No. 12;

RESULT 864
ID   AAR53748 standard; protein; 355 AA.
DE   Seven transmembrane receptor (V28).
PN   WO9412635-A2.
PD   09-JUN-1994.
PA   (ICOS-) ICOS CORP.
Query Match   6.2%;   Score 74.5; DB 2; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;

RESULT 865
ID   AAW48722 standard; protein; 355 AA.
DE   Human V28 seven transmembrane receptor.
PN   US5759804-A.
PD   02-JUN-1998.
PA   (ICOS-) ICOS CORP.
Query Match   6.2%;   Score 74.5; DB 2; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;

RESULT 866
ID   AAY90677 standard; protein; 355 AA.
DE   Human mutant G protein-coupled receptor V28 (1230K).
PN   WO200022129-A1.
PD   20-APR-2000.
PA   (AREN-) ARENA PHARM INC.
Query Match   6.2%;   Score 74.5; DB 3; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;

RESULT 867
ID   AAY90642 standard; protein; 355 AA.
DE   Human G protein-coupled receptor V28.
PN   WO200022129-A1.
PD   20-APR-2000.
PA   (AREN-) ARENA PHARM INC.
Query Match   6.2%;   Score 74.5; DB 3; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;

RESULT 868
ID   AAB21693 standard; protein; 355 AA.
DE   Human 7TM receptor V28 cDNA clone protein #2.
PN   US6107475-A.
PD   22-AUG-2000.
PA   (ICOS-) ICOS CORP.
Query Match   6.2%;   Score 74.5; DB 3; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;

RESULT 869
ID   AAB21692 standard; protein; 355 AA.
DE   Human 7TM receptor V28 cDNA clone protein #1.
PN   US6107475-A.
PD   22-AUG-2000.
PA   (ICOS-) ICOS CORP.
Query Match   6.2%;   Score 74.5; DB 3; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;

RESULT 870
ID   AAB80126 standard; protein; 355 AA.
DE   Human CX3CR1 protein.
PN   WO200172830-A2.
PD   04-OCT-2001.
PA   (IPPF-) IPF PHARM GMBH.
PA   (FORS/) FORSSMANN U.
Query Match   6.2%;   Score 74.5; DB 4; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;

RESULT 871
ID   AAB82786 standard; protein; 355 AA.
DE   Human CX3C chemokine receptor 1.
PN   WO200160406-A1.
PD   23-AUG-2001.
PA   (MILL-) MILLENNIUM PHARM INC.
PA   (NOUN) UNIV NORTHWESTERN.
Query Match   6.2%;   Score 74.5; DB 4; Length 355;
Best Local Similarity 25.8%; Pred. No. 19;

RESULT 872

ID   AAU91235 standard; protein; 355 AA.
DE   Human 7 transmembrane domain receptor V28 #2.
PN   US6348574-B1.
PD   19-FEB-2002.
PA   (ICOS-) ICOS CORP.
     Query Match
     Best Local Similarity   25.8%;   6.2%;   Score 74.5;   DB 5;   Length 355;
                                               Pred. No. 19;
RESULT 873
ID   AAU91234 standard; protein; 355 AA.
DE   Human 7 transmembrane domain receptor V28 #1.
PN   US6348574-B1.
PD   19-FEB-2002.
PA   (ICOS-) ICOS CORP.
     Query Match
     Best Local Similarity   25.8%;   6.2%;   Score 74.5;   DB 5;   Length 355;
                                               Pred. No. 19;
RESULT 874
ID   AAU84327 standard; protein; 355 AA.
DE   Protein CX3CR1 differentially expressed in breast cancer tissue.
PN   WO200210436-A2.
PD   07-FEB-2002.
PA   (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
PA   (BAAK/) BAAK J.
     Query Match
     Best Local Similarity   25.8%;   6.2%;   Score 74.5;   DB 5;   Length 355;
                                               Pred. No. 19;
RESULT 875
ID   ABR58524 standard; protein; 355 AA.
DE   Human chemokine (C-X3-C) receptor 1 protein.
PN   WO200302518-A2.
PD   27-MAR-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
     Query Match
     Best Local Similarity   25.8%;   6.2%;   Score 74.5;   DB 5;   Length 355;
                                               Pred. No. 19;
RESULT 876
ID   AAO29513 standard; protein; 355 AA.
DE   Human fractalkine receptor (313) protein.
PN   WO200303475-A2.
PD   15-MAY-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match
     Best Local Similarity   25.8%;   6.2%;   Score 74.5;   DB 6;   Length 355;
                                               Pred. No. 19;
RESULT 877
ID   ABP97732 standard; protein; 355 AA.
DE   Amino acid sequence of human chemokine receptor CX3CR1.
PN   WO200301415-A2.
PD   20-FEB-2003.
PA   (TOPI-) TOPIGEN PHARM INC.
     Query Match
     Best Local Similarity   25.8%;   6.2%;   Score 74.5;   DB 6;   Length 355;
                                               Pred. No. 19;
RESULT 878
ID   ABP81882 standard; protein; 355 AA.
DE   Human CX3C chemokine fractalkine receptor 1 protein SEQ ID NO:249.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
     Query Match
     Best Local Similarity   25.8%;   6.2%;   Score 74.5;   DB 6;   Length 355;
                                               Pred. No. 19;
RESULT 879
ID   ADC22751 standard; protein; 355 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #74.
PN   US6555339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
     Query Match
     Best Local Similarity   25.8%;   6.2%;   Score 74.5;   DB 7;   Length 355;
                                               Pred. No. 19;
RESULT 880
ID   ADC22649 standard; protein; 355 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #34.
PN   US6555339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
     Query Match
     Best Local Similarity   25.8%;   6.2%;   Score 74.5;   DB 7;   Length 355;
                                               Pred. No. 19;
RESULT 881

ID   ADH14224 standard; protein; 355 AA.
DE   Mutated human serotonin V28.
PN   US2003105292-A1.
PD   05-JUN-2003.
PA   (LIAW/) LIAW C W.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.
     Query Match
     Best Local Similarity   25.8%;   6.2%;   Score 74.5;   DB 7;   Length 355;
                                               Pred. No. 19;
RESULT 882
ID   ADH14122 standard; protein; 355 AA.
DE   Human serotonin V28.
PN   US2003105292-A1.
PD   05-JUN-2003.
PA   (LIAW/) LIAW C W.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.
     Query Match
     Best Local Similarity   25.8%;   6.2%;   Score 74.5;   DB 7;   Length 355;
                                               Pred. No. 19;
RESULT 883
ID   ADH10680 standard; protein; 355 AA.
DE   Human CX3CR1 polypeptide.
PN   WO200310484-A1.
PD   18-DEC-2003.
PA   (META-) METABOLEX INC.
     Query Match
     Best Local Similarity   25.8%;   6.2%;   Score 74.5;   DB 8;   Length 355;
                                               Pred. No. 19;
RESULT 884
ID   ADO22269 standard; protein; 355 AA.
DE   Human GPCR CX3CR1, SEQ ID NO:370.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
     Query Match
     Best Local Similarity   25.8%;   6.2%;   Score 74.5;   DB 8;   Length 355;
                                               Pred. No. 19;
RESULT 885
ID   ADQ18141 standard; protein; 355 AA.
DE   Human soft tissue sarcoma-upregulated protein - SEQ ID 958.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
     Query Match
     Best Local Similarity   25.8%;   6.2%;   Score 74.5;   DB 8;   Length 355;
                                               Pred. No. 19;
RESULT 886
ID   ADP56020 standard; protein; 355 AA.
DE   Human PRO protein sequence SEQ ID NO:1996.
PN   WO2004039956-A2.
PD   13-MAY-2004.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   25.8%;   6.2%;   Score 74.5;   DB 8;   Length 355;
                                               Pred. No. 19;
RESULT 887
ID   ADP54585 standard; protein; 355 AA.
DE   Human PRO protein sequence SEQ ID NO:561.
PN   WO2004039956-A2.
PD   13-MAY-2004.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   25.8%;   6.2%;   Score 74.5;   DB 8;   Length 355;
                                               Pred. No. 19;
RESULT 888
ID   ADP23931 standard; protein; 355 AA.
DE   PRO polypeptide SEQ ID NO:1109.
PN   WO2004041170-A2.
PD   21-MAY-2004.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity   25.8%;   6.2%;   Score 74.5;   DB 8;   Length 355;
                                               Pred. No. 19;
RESULT 889
ID   ADQ39421 standard; protein; 355 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1084.
PN   WO2004050052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.

Query Match
Best Local Similarity   25.8%;   Score 74.5;   DB 8;   Pred. No. 19;   Length 355;
RESULT 890
ID   ADY15644 standard; protein; 355 AA.
DE   PRO polypeptide SEQ ID NO 1450.
PN   WO2005016962-A2.
PD   24-FEB-2005.
PA   (GETH) GENENTECH INC.

Query Match
Best Local Similarity   25.8%;   Score 74.5;   DB 9;   Pred. No. 19;   Length 355;
RESULT 891
ID   AED67635 standard; protein; 355 AA.
DE   Human CX3C chemokine receptor 1 (CX3CR1).
PN   WO2005103684-A2.
PD   03-NOV-2005.
PA   (APPL-) APPLERA CORP.

Query Match
Best Local Similarity   25.8%;   Score 74.5;   DB 9;   Pred. No. 19;   Length 362;
RESULT 892
ID   ADQ39422 standard; protein; 362 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1085.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (TEIT/) TEITLER M.
PA   (HERR/) HERRICK-DAVIS K.
PA   (EGAN/) EGAN C C.

Query Match
Best Local Similarity   21.0%;   Score 74.5;   DB 2;   Pred. No. 28;   Length 471;
RESULT 893
ID   AAW77109 standard; protein; 471 AA.
DE   Rat 5-HT2A serotonin receptor C322K mutant.
PN   WO9838217-A1.
PD   03-SEP-1998.
PA   (TEIT/) TEITLER M.
PA   (HERR/) HERRICK-DAVIS K.
PA   (EGAN/) EGAN C C.

Query Match
Best Local Similarity   21.0%;   Score 74.5;   DB 2;   Pred. No. 28;   Length 471;
RESULT 894
ID   AAW77111 standard; protein; 471 AA.
DE   Rat 5-HT2A serotonin receptor C322E mutant.
PN   WO9838217-A1.
PD   03-SEP-1998.
PA   (TEIT/) TEITLER M.
PA   (HERR/) HERRICK-DAVIS K.
PA   (EGAN/) EGAN C C.

Query Match
Best Local Similarity   21.0%;   Score 74.5;   DB 2;   Pred. No. 28;   Length 471;
RESULT 895
ID   AAW77110 standard; protein; 471 AA.
DE   Rat 5-HT2A serotonin receptor C322R mutant.
PN   WO9838217-A1.
PD   03-SEP-1998.
PA   (TEIT/) TEITLER M.
PA   (HERR/) HERRICK-DAVIS K.
PA   (EGAN/) EGAN C C.

Query Match
Best Local Similarity   21.0%;   Score 74.5;   DB 2;   Pred. No. 28;   Length 471;
RESULT 896
ID   AAW77104 standard; protein; 471 AA.
DE   Rat 5-HT2A serotonin receptor.
PN   WO9838217-A1.
PD   03-SEP-1998.
PA   (TEIT/) TEITLER M.
PA   (HERR/) HERRICK-DAVIS K.
PA   (EGAN/) EGAN C C.

Query Match
Best Local Similarity   21.0%;   Score 74.5;   DB 5;   Pred. No. 28;   Length 471;
RESULT 897
ID   ABB07980 standard; protein; 471 AA.
DE   Rat 5-HT2 receptor sequence.
PN   US6383762-B1.
PD   07-MAY-2002.
PA   (SYNA-) SYNAPTIC PHARM CORP.

Query Match
Best Local Similarity   21.0%;   Score 74.5;   DB 8;   Pred. No. 28;   Length 481;
RESULT 898
ID   ADF74971 standard; protein; 481 AA.
DE   Rat 164-1b protein (SeqID 30).
PN   WO2003097686-A1.
PD   27-NOV-2003.
PA   (TAKE) TAKEDA CHEM IND LTD.

Query Match
Best Local Similarity   23.3%;   Score 74.5;   DB 4;   Pred. No. 29;   Length 481;
RESULT 899
ID   AAM93692 standard; protein; 562 AA.
DE   Human polypeptide, SEQ ID NO: 3602.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.

Query Match
Best Local Similarity   23.1%;   Score 74.5;   DB 8;   Pred. No. 36;   Length 562;
RESULT 900
ID   ADJ31569 standard; protein; 562 AA.
DE   Human protein encoded by a full length cDNA clone SeqID 3602.
PN   EP1396543-A2.
PD   10-MAR-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.

Query Match
Best Local Similarity   23.1%;   Score 74.5;   DB 8;   Pred. No. 36;   Length 562;
RESULT 901
ID   ADQ96118 standard; protein; 562 AA.
DE   T cell activation associated gene protein #158.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.

Query Match
Best Local Similarity   23.0%;   Score 74.5;   DB 8;   Pred. No. 36;   Length 587;
RESULT 902
ID   ADR86160 standard; protein; 587 AA.
DE   Aspergillus fumigatus essential gene protein #210.
PN   WO2004067709-A2.
PD   12-AUG-2004.
PA   (ELIT-) ELITRA PHARM INC.
PA   (ELIT-) ELITRA CANADA LTD.

Query Match
Best Local Similarity   18.2%;   Score 74.5;   DB 8;   Pred. No. 38;   Length 597;
RESULT 903
ID   ABB62948 standard; protein; 597 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 15636.
PN   WO2001071042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.

Query Match
Best Local Similarity   27.2%;   Score 74.5;   DB 4;   Pred. No. 39;   Length 661;
RESULT 904
ID   ADX66440 standard; protein; 661 AA.
DE   Plant full length insert polypeptide seqid 37283.
PN   US20040034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.

Query Match
Best Local Similarity   20.4%;   Score 74.5;   DB 8;   Pred. No. 45;   Length 940;
RESULT 905
ID   ADA36878 standard; protein; 940 AA.
DE   Acinetobacter baumannii protein #4039.
PN   US6562958-B1.
PD   13-MAY-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.

Query Match
Best Local Similarity   21.1%;   Score 74.5;   DB 6;   Pred. No. 73;   Length 1808;
RESULT 906
ID   ABB92731 standard; protein; 1808 AA.

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DE   Herbicidally active polypeptide SEQ ID NO 1942.
PN   WO200210210-A2.
PD   07-FEB-2002.
PA   (FARB ) BAYER AG.
RESULT 907
Best Local Similarity   17.3%;
  Query Match   6.2%;   Score 74.5;  DB 5;  Length 1808;
ID   AAE20477 standard; protein; 3010 AA.
DE   HCV-S1 full-length polyprotein.
PN   WO20020447-A2.
PD   31-JAN-2002.
PA   (MOLE/) INST MOLECULAR & CELL BIOLOGY.
PA   (EHRL/) EHRLICH G.
RESULT 908
Best Local Similarity   23.8%;
  Query Match   6.2%;   Score 74.5;  DB 5;  Length 3010;
ID   ADF07294 standard; protein; 154 AA.
DE   Bacterial polypeptide #3407.
PN   US605709-B1.
PD   12-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
RESULT 909
Best Local Similarity   26.4%;
  Query Match   6.2%;   Score 74;  DB 7;  Length 154;
ID   ABU70365 standard; protein; 231 AA.
DE   Human adipocyte bait protein, melatonin receptor_V4.
PN   WO200286122-A2.
PD   31-OCT-2002.
PA   (HYBR-) HYBRIGENICS.
RESULT 910
Best Local Similarity   18.5%;
  Query Match   6.2%;   Score 74;  DB 6;  Length 231;
ID   ABU70366 standard; protein; 231 AA.
DE   Human adipocyte bait protein, melatonin receptor_V5.
PN   WO200286122-A2.
PD   31-OCT-2002.
PA   (HYBR-) HYBRIGENICS.
RESULT 911
Best Local Similarity   18.5%;
  Query Match   6.2%;   Score 74;  DB 6;  Length 231;
ID   ABB54180 standard; protein; 312 AA.
DE   Lactococcus lactis protein yiiG.
PN   FR287446-A1.
PD   12-OCT-2001.
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
RESULT 912
Best Local Similarity   24.3%;
  Query Match   6.2%;   Score 74;  DB 5;  Length 312;
ID   ADS44483 standard; protein; 312 AA.
DE   Bacterial polypeptide #22913.
PN   US200323675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
RESULT 913
Best Local Similarity   38.3%;
  Query Match   6.2%;   Score 74;  DB 8;  Length 312;
ID   ABU02869 standard; protein; 324 AA.
DE   S. pneumoniae type 4 strain protein from coding region #2450.
PN   WO20027021-A2.
PD   03-OCT-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
RESULT 914
Best Local Similarity   24.3%;
  Query Match   6.2%;   Score 74;  DB 6;  Length 324;
ID   ADR94027 standard; protein; 332 AA.
DE   Novel S. pneumoniae protein sequence, SEQ ID 2662.
PN   US600744-B1.
PD   05-OCT-2004.

PA   (GENO-) GENOME THERAPEUTICS CORP.
RESULT 915
Best Local Similarity   24.3%;
  Query Match   6.2%;   Score 74;  DB 8;  Length 332;
ID   AEA57897 standard; protein; 332 AA.
DE   Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:2662.
PN   US2005136404-A1.
PD   23-JUN-2005.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.
RESULT 916
Best Local Similarity   24.3%;
  Query Match   6.2%;   Score 74;  DB 9;  Length 332;
ID   AB000448 standard; protein; 342 AA.
DE   Novel human polypeptide #35.
PN   WO2003023013-A2.
PD   20-MAR-2003.
PA   (HYSE-) HYSEQ INC.
RESULT 917
Best Local Similarity   21.2%;
  Query Match   6.2%;   Score 74;  DB 6;  Length 342;
ID   AAR88412 standard; protein; 350 AA.
DE   High-affinity melatonin melatonin-1a receptor.
PN   WO9535320-A1.
PD   28-DEC-1995.
PA   (MASS-) MASSACHUSETTS GEN HOSPITAL.
RESULT 918
Best Local Similarity   18.5%;
  Query Match   6.2%;   Score 74;  DB 2;  Length 350;
ID   AAW15786 standard; protein; 350 AA.
DE   Melatonin receptor protein.
PN   JP09084581-A.
PD   31-MAR-1997.
PA   (TAKE ) TAKEDA CHEM IND LTD.
RESULT 919
Best Local Similarity   18.5%;
  Query Match   6.2%;   Score 74;  DB 2;  Length 350;
ID   AAW94761 standard; protein; 350 AA.
DE   Human melatonin receptor protein mel-1a.
PN   EP892046-A2.
PD   20-JAN-1999.
PA   (JCRP-) JCR PHARM CO LTD.
RESULT 920
Best Local Similarity   18.5%;
  Query Match   6.2%;   Score 74;  DB 2;  Length 350;
ID   ABP81840 standard; protein; 350 AA.
DE   Human melatonin receptor type 1a protein mel-1a.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
RESULT 921
Best Local Similarity   18.5%;
  Query Match   6.2%;   Score 74;  DB 6;  Length 350;
ID   ADO29552 standard; protein; 350 AA.
DE   Human GPCR MTNR1A, SEQ ID NO:654.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
RESULT 922
Best Local Similarity   18.5%;
  Query Match   6.2%;   Score 74;  DB 8;  Length 350;
ID   AEC08362 standard; protein; 350 AA.
DE   Human melatonin receptor type 1A (MTNR1A).
PN   WO2005078455-A1.
PD   25-AUG-2005.
PA   (FARB ) BAYER HEALTHCARE AG.
RESULT 923
Best Local Similarity   18.5%;
  Query Match   6.2%;   Score 74;  DB 9;  Length 350;
ID   AAW12220 standard; protein; 364 AA.
DE   Rat growth hormone secretagogue receptor type Ia.
PN   WO9721730-A1.
PD   19-JUN-1997.
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PA   (MERI) MERCK & CO INC.
      Query Match   6.2%;
      Best Local Similarity 19.4%;   Score 74;   Pred. No. 22;   DB 2;   Length 364;

RESULT 924
ID   ABM73179 standard; protein; 366 AA.
DE   Staphylococcus aureus protein #2419.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
      Query Match   6.2%;
      Best Local Similarity 21.8%;   Score 74;   Pred. No. 23;   DB 6;   Length 366;

RESULT 925
ID   ABB55224 standard; protein; 442 AA.
DE   Lactococcus lactis protein yteD.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG) INRA INST NAT RECH AGRONOMIQUE.
      Query Match   6.2%;
      Best Local Similarity 20.4%;   Score 74;   Pred. No. 29;   DB 5;   Length 442;

RESULT 926
ID   ADN23927 standard; protein; 485 AA.
DE   Bacterial polypeptide #6580.
PN   US200323675-A1.
PD   18-DEC-2003.
PA   (GOLD/) GOLDMAN B S.
      Query Match   6.2%;
      Best Local Similarity 26.2%;   Score 74;   Pred. No. 33;   DB 8;   Length 485;

RESULT 927
ID   AAY80509 standard; protein; 492 AA.
DE   F. lutescens L-lysine:2-oxoglutarate 6-aminotransferase.
PN   WO200008170-A1.
PD   17-FEB-2000.
PA   (SACC) MERCIAN CORP.
      Query Match   6.2%;
      Best Local Similarity 22.5%;   Score 74;   Pred. No. 34;   DB 3;   Length 492;

RESULT 928
ID   AAG64105 standard; protein; 493 AA.
DE   Flavobacterium lutescens L-lysine-6-aminotransferase.
PN   WO200148216-A1.
PD   05-JUL-2001.
PA   (SACC) MERCIAN CORP.
      Query Match   6.2%;
      Best Local Similarity 22.5%;   Score 74;   Pred. No. 34;   DB 4;   Length 493;

RESULT 929
ID   AAR54067 standard; protein; 1031 AA.
DE   Non-A, non-B hepatitis virus gene #6 product.
PN   JP06141870-A.
PD   24-MAY-1994.
PA   (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
PA   (SANW) SANWA KAGAKU KENKYUSHO CO.
PA   (TOFU) TONEN CORP.
      Query Match   6.2%;
      Best Local Similarity 26.2%;   Score 74;   Pred. No. 95;   DB 2;   Length 1031;

RESULT 930
ID   AAR98362 standard; protein; 1031 AA.
DE   5'-UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#6).
PN   JP07133291-A.
PD   23-MAY-1995.
PA   (TOFU) TONEN CORP.
      Query Match   6.2%;
      Best Local Similarity 26.2%;   Score 74;   Pred. No. 95;   DB 2;   Length 1031;

RESULT 931
ID   AAG59839 standard; protein; 120 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 77442.
PN   EP1033405-A2.
PD   06-SEP-2000.
      Query Match   6.2%;
      Best Local Similarity 20.3%;   Score 73.5;   Pred. No. 5.5;   DB 3;   Length 120;

RESULT 932
ID   AAU25578 standard; protein; 192 AA.
DE   Human G Protein-Coupled Receptor (GPCR) polypeptide #25.
PN   WO200162797-A2.
PD   30-AUG-2001.
PA   (PHAA) PHARMACIA & UPJOHN CO.
      Query Match   6.2%;
      Best Local Similarity 26.3%;   Score 73.5;   Pred. No. 11;   DB 4;   Length 192;

RESULT 933
ID   ADU08915 standard; protein; 226 AA.
DE   Coronavirus membrane protein seqid 38.
PN   WO200496842-A2.
PD   11-NOV-2004.
PA   (BCCA-) BC CANCER AGENCY.
      Query Match   6.2%;
      Best Local Similarity 22.2%;   Score 73.5;   Pred. No. 13;   DB 8;   Length 226;

RESULT 934
ID   ABU44044 standard; protein; 268 AA.
DE   Protein encoded by Prokaryotic essential gene #29571.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
      Query Match   6.2%;
      Best Local Similarity 19.6%;   Score 73.5;   Pred. No. 17;   DB 6;   Length 268;

RESULT 935
ID   AAG32488 standard; protein; 282 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 39200.
PN   EP1033405-A2.
PD   06-SEP-2000.
      Query Match   6.2%;
      Best Local Similarity 28.1%;   Score 73.5;   Pred. No. 18;   DB 3;   Length 282;

RESULT 936
ID   ADF05982 standard; protein; 312 AA.
DE   Bacterial polypeptide #2095.
PN   US6605709-B1.
PD   12-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
      Query Match   6.2%;
      Best Local Similarity 17.4%;   Score 73.5;   Pred. No. 21;   DB 7;   Length 312;

RESULT 937
ID   AAG51386 standard; protein; 377 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 65212.
PN   EP1033405-A2.
PD   06-SEP-2000.
      Query Match   6.2%;
      Best Local Similarity 28.1%;   Score 73.5;   Pred. No. 27;   DB 3;   Length 377;

RESULT 938
ID   AAG32487 standard; protein; 377 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 39199.
PN   EP1033405-A2.
PD   06-SEP-2000.
      Query Match   6.2%;
      Best Local Similarity 28.1%;   Score 73.5;   Pred. No. 27;   DB 3;   Length 377;

RESULT 939
ID   ABM92289 standard; protein; 400 AA.
DE   M. xanthus protein sequence, seq id 11488.
PN   US6833447-B1.
PD   21-DEC-2004.
PA   (MONS) MONSANTO TECHNOLOGY LLC.
      Query Match   6.2%;
      Best Local Similarity 23.3%;   Score 73.5;   Pred. No. 29;   DB 9;   Length 400;

RESULT 940
ID   ADQ75734 standard; protein; 404 AA.
DE   Codon optimised hCMV IE1 encoded exons 2 and 4.
PN   WO200405816-A2.
PD   15-JUL-2004.
PA   (VICA-) VICAL INC.
      Query Match   6.2%;
      Best Local Similarity 19.3%;   Score 73.5;   Pred. No. 30;   DB 8;   Length 404;

RESULT 941
ID   AAG51385 standard; protein; 442 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 65211.
PN   EP1033405-A2.
PD   06-SEP-2000.

RESULT 942
Query Match 28.1%; Best Local Similarity 6.2%; Score 73.5; Pred. No. 34; DB 3; Length 442;
ID AAG32486 standard; protein; 442 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39198.
PN EP1033405-A2.
PD 06-SEP-2000.

RESULT 943
Query Match 28.1%; Best Local Similarity 6.2%; Score 73.5; Pred. No. 34; DB 3; Length 442;
ID AAG51384 standard; protein; 489 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65210.
PN EP1033405-A2.
PD 06-SEP-2000.

RESULT 944
Query Match 28.1%; Best Local Similarity 6.2%; Score 73.5; Pred. No. 39; DB 3; Length 489;
ID AAB86544 standard; protein; 491 AA.
DE Human cytomegalovirus strain AD169 IE1 protein.
PN WO200163286-A2.
PD 30-AUG-2001.
PA (KERN/) KERN F.

RESULT 945
Query Match 19.3%; Best Local Similarity 6.2%; Score 73.5; Pred. No. 39; DB 4; Length 491;
ID ADP12517 standard; protein; 491 AA.
DE Protein encoded by mRNA of the invention #127.
PN WO200404346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.

RESULT 946
Query Match 19.3%; Best Local Similarity 6.2%; Score 73.5; Pred. No. 39; DB 8; Length 491;
ID ADP12518 standard; protein; 491 AA.
DE Protein encoded by mRNA of the invention #128.
PN WO200404346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.

RESULT 947
Query Match 19.3%; Best Local Similarity 6.2%; Score 73.5; Pred. No. 39; DB 8; Length 491;
ID ADP12513 standard; protein; 491 AA.
DE Protein encoded by mRNA of the invention #123.
PN WO200404346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.

RESULT 948
Query Match 19.3%; Best Local Similarity 6.2%; Score 73.5; Pred. No. 39; DB 8; Length 491;
ID ADP12514 standard; protein; 491 AA.
DE Protein encoded by mRNA of the invention #124.
PN WO200404346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.

RESULT 949
Query Match 19.3%; Best Local Similarity 6.2%; Score 73.5; Pred. No. 39; DB 8; Length 491;
ID ADQ75725 standard; protein; 491 AA.
DE Wild type hCMV IE1.
PN WO200405816-A2.
PD 15-JUL-2004.
PA (VICA/) VICAL INC.

RESULT 950
Query Match 19.3%; Best Local Similarity 6.2%; Score 73.5; Pred. No. 48; DB 8; Length 491;
ID ABP7574 standard; protein; 574 AA.
DE Candida albicans essential protein SEQ ID NO 7411.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.

RESULT 951
Query Match 20.8%; Best Local Similarity 6.2%; Score 73.5; Pred. No. 48; DB 5; Length 574;
ID AED26251 standard; protein; 577 AA.
DE Novel human full-length polypeptide 791CIP22B_12, SEQ ID NO:247.
PN US2005221342-A1.
PD 06-OCT-2005.
PA (NUVE-) NUVELO INC.

RESULT 952
Query Match 20.8%; Best Local Similarity 6.2%; Score 73.5; Pred. No. 49; DB 9; Length 577;
ID ADS28278 standard; protein; 637 AA.
DE Bacterial polypeptide #17311.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

RESULT 953
Query Match 28.3%; Best Local Similarity 6.2%; Score 73.5; Pred. No. 56; DB 8; Length 637;
ID ABG29128 standard; protein; 682 AA.
DE Novel human diagnostic protein #29119.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.

RESULT 954
Query Match 28.3%; Best Local Similarity 6.2%; Score 73.5; Pred. No. 62; DB 4; Length 682;
ID ABB61737 standard; protein; 1287 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12003.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

RESULT 955
Query Match 20.0%; Best Local Similarity 6.2%; Score 73.5; Pred. No. 1.5e+02; DB 4; Length 1287;
ID ADS96670 standard; protein; 1287 AA.
DE Drosophila melanogaster protein, SEQ ID 291.
PN WO2004039999-A2.
PD 13-MAY-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

RESULT 956
Query Match 18.2%; Best Local Similarity 6.2%; Score 73.5; Pred. No. 1.5e+02; DB 8; Length 1287;
ID AAR33214 standard; protein; 3033 AA.
DE NANBH virus strain HC-J8 protein.
PN EP532167-A2.
PD 17-MAR-1993.
PA (IMMO) IMMUNO JAPAN INC.

RESULT 957
Query Match 27.4%; Best Local Similarity 6.2%; Score 73.5; Pred. No. 1.5e+02; DB 2; Length 3033;
ID ABY03151 standard; protein; 7176 AA.
DE Murine hepatitis virus pol1ab protein, SEQ:9897.
PN WO200409360-A2.
PD 28-OCT-2004.
PA (CHIR) CHIRON CORP.

RESULT 958
Query Match 26.4%; Best Local Similarity 6.2%; Score 73.5; Pred. No. 1.6e+03; DB 8; Length 7176;
ID AAW20571 standard; protein; 114 AA.
DE H. pylori secreted or periplasmic protein 80257.aa.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.

RESULT 959
Query Match 21.6%; Best Local Similarity 6.1%; Score 73; Pred. No. 5.9; DB 2; Length 114;
ID AAU69567 standard; protein; 189 AA.
DE Human G protein-coupled receptor from cDNA Seq-2643.
PN WO200177330-A2.
PD 18-OCT-2001.
PA (PHAA) PHARMACIA & UPJOHN CO.

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Query Match
Best Local Similarity        20.3%;   Score 73;   Pred. No. 12;   DB 5;   Length 189;
RESULT 960
ID   ADC97146 standard; protein; 199 AA.
DE   E. faecium protein sequence SEQ ID 6773.
PN   US6583275-B1.
PD   24-JUN-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
PA   (CHIR-) CHIRON SPA.
PA   (ABBO ) ABBOTT LAB.

Query Match
Best Local Similarity        22.6%;   Score 73;   Pred. No. 13;   DB 7;   Length 199;
RESULT 961
ID   ABP29367 standard; protein; 249 AA.
DE   Streptococcus polypeptide SEQ ID NO 7910.
PN   WO200234771-A2.
PD   02-MAY-2002.
PA   (GENO-) INST GENOMIC RES.

Query Match
Best Local Similarity        24.6%;   Score 73;   Pred. No. 17;   DB 5;   Length 249;
RESULT 962
ID   AAU87836 standard; protein; 272 AA.
DE   T. aureum 7091 elongase TEL01 from plasmid pRAT-4-A1.
PN   WO200208401-A2.
PD   31-JAN-2002.
PA   (ABBO ) ABBOTT LAB.

Query Match
Best Local Similarity        19.9%;   Score 73;   Pred. No. 20;   DB 5;   Length 272;
RESULT 963
ID   ADH80191 standard; protein; 272 AA.
DE   Fungal 7091 elongase protein seq id 75.
PN   US20030163845-A1.
PD   28-AUG-2003.
PA   (MUKE/) MUKERJI P.
PA   (LEON/) EUN-YEONG LEONARD A.
PA   (HUAN/) HUANG Y.
PA   (PERE/) PEREIRA S L.

Query Match
Best Local Similarity        19.9%;   Score 73;   Pred. No. 20;   DB 8;   Length 272;
RESULT 964
ID   ADW12982 standard; protein; 272 AA.
DE   Elongase protein #55.
PN   US200509140-A1.
PD   13-JAN-2005.
PA   (MUKE/) MUKERJI P.
PA   (LEON/) LEONARD A E.
PA   (HUAN/) HUANG Y.
PA   (PERE/) PEREIRA S L.

Query Match
Best Local Similarity        19.9%;   Score 73;   Pred. No. 20;   DB 9;   Length 272;
RESULT 965
ID   ABM73154 standard; protein; 290 AA.
DE   Staphylococcus aureus protein #2394.
PN   WO200294868-A2.
PD   28-NOV-2002.

Query Match
Best Local Similarity        23.4%;   Score 73;   Pred. No. 22;   DB 6;   Length 290;
RESULT 966
ID   ABR47464 standard; protein; 322 AA.
DE   Breast cancer associated protein sequence SEQ ID NO:160.
PN   WO200304989-A2.
PD   16-JAN-2003.
PA   (MILL-) MILLENIUM PHARM INC.

Query Match
Best Local Similarity        20.6%;   Score 73;   Pred. No. 25;   DB 6;   Length 322;
RESULT 967
ID   ADN61865 standard; protein; 349 AA.
DE   Human novel protein NOV42a.
PN   US200404382-A1.
PD   04-MAR-2004.
PA   (PADI/) PADIGARU M.
PA   (SPYT/) SPYTEK K A.
PA   (SHEN/) SHENOY S G.
PA   (TAUP/) TAUPIER R J.
PA   (PENA/) PENA C E A.
PA   (LILL/) LI L.
PA   (ZERH/) ZERHUSEN B D.
PA   (GUSE/) GUSEV V Y.
PA   (JIWW/) JI W.
PA   (GORM/) GORMAN L.
PA   (MILL/) MILLER C E.
PA   (KEKU/) KEKUDA R.
PA   (PATT/) PATTURAJAN M.
PA   (GANG/) GANGOLLI E A.
PA   (VERN/) VERNET C A M.
PA   (GUOX/) GUO X S.
PA   (TCHE/) TCHERNEV V T.
PA   (FERN/) FERNANDES E R.
PA   (CASM/) CASMAN S J.
PA   (MALY/) MALYANKAR U M.
PA   (GERL/) GERLACH V.
PA   (LIUY/) LIU Y.
PA   (ANDE/) ANDERSON D W.
PA   (SPAD/) SPADERNA S K.
PA   (CATT/) CATTERTON E.
PA   (LEIT/) LEITE M W.
PA   (ZHON/) ZHONG H
PA   (ALSO/) ALSOBROOK J P.
PA   (LEPL/) LEPLEY D M.
PA   (RIEG/) RIEGER D K.
PA   (BURG/) BURGESS C E.

Query Match
Best Local Similarity        24.0%;   Score 73;   Pred. No. 28;   DB 8;   Length 349;
RESULT 968
ID   AAW19613 standard; protein; 364 AA.
DE   Rat growth hormone secretagogue receptor type Ia.
PN   WO9722004-A1.
PD   19-JUN-1997.
PA   (MERI ) MERCK & CO INC.

Query Match
Best Local Similarity        19.4%;   Score 73;   Pred. No. 29;   DB 2;   Length 364;
RESULT 969
ID   AAY54565 standard; protein; 364 AA.
DE   A mouse growth hormone secretagogue receptor.
PN   WO2002002918-A1.
PD   20-JAN-2000.
PA   (MERI ) MERCK & CO INC.

Query Match
Best Local Similarity        19.4%;   Score 73;   Pred. No. 29;   DB 3;   Length 364;
RESULT 970
ID   AAB97377 standard; protein; 364 AA.
DE   Rat growth hormone secretagogue receptor (GHSR) related protein.
PN   WO200132705-A1.
PD   10-MAY-2001.
PA   (TAKE ) TAKEDA CHEM IND LTD.

Query Match
Best Local Similarity        19.4%;   Score 73;   Pred. No. 29;   DB 4;   Length 364;
RESULT 971
ID   ADO29026 standard; protein; 364 AA.
DE   Mouse novel GPCR GHSR, SEQ ID NO:125.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.

Query Match
Best Local Similarity        19.4%;   Score 73;   Pred. No. 29;   DB 8;   Length 364;
RESULT 972
ID   AAW77773 standard; protein; 377 AA.
DE   Staphylococcus aureus protein of unknown function.
PN   EP841394-A2.
PD   13-MAY-1998.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.

Query Match
Best Local Similarity        23.3%;   Score 73;   Pred. No. 31;   DB 2;   Length 377;
RESULT 973
ID   AAG50065 standard; protein; 415 AA.
```

DE Arabidopsis thaliana protein fragment SEQ ID NO: 63404.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (ELIT-) ELITRA PHARM INC.

RESULT 974
Query Match
Best Local Similarity 6.1%; 19.8%;
Score 73; DB 3; Length 427; Pred. No. 35;
ID AAG24013 standard; protein; 427 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27528.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (ELIT-) ELITRA PHARM INC.

RESULT 975
Query Match
Best Local Similarity 6.1%; 22.0%;
Score 73; DB 3; Length 430; Pred. No. 37;
ID AAG24012 standard; protein; 430 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27527.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (ELIT-) ELITRA PHARM INC.

RESULT 976
Query Match
Best Local Similarity 6.1%; 26.5%;
Score 73; DB 9; Length 453; Pred. No. 40;
ID ABU31419 standard; protein; 453 AA.
DE Protein encoded by Prokaryotic essential gene #16946.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (CURA-) CURAGEN CORP.

RESULT 977
Query Match
Best Local Similarity 6.1%; 19.8%;
Score 73; DB 6; Length 469; Pred. No. 42;
ID AEA16981 standard; protein; 469 AA.
DE Arabidopsis thaliana protein #40.
PN US2005125159-A1.
PD 09-JUN-2005.
PA (STEI/) STEIN J C.
PA (CAOY/) CAO Y.

RESULT 978
Query Match
Best Local Similarity 6.1%; 19.8%;
Score 73; DB 3; Length 472; Pred. No. 43;
ID AAG50064 standard; protein; 472 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63403.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (ELIT-) ELITRA PHARM INC.

RESULT 979
Query Match
Best Local Similarity 6.1%; 19.8%;
Score 73; DB 3; Length 474; Pred. No. 45;
ID AAG50063 standard; protein; 474 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63402.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (ELIT-) ELITRA PHARM INC.

RESULT 980
Query Match
Best Local Similarity 6.1%; 19.8%;
Score 73; DB 6; Length 490; Pred. No. 45;
ID ABM70313 standard; protein; 490 AA.
DE Photorhabdus luminescens protein sequence #3410.
PN WO2002094867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.

RESULT 981
Query Match
Best Local Similarity 6.1%; 24.6%;
Score 73; DB 2; Length 495; Pred. No. 45;
ID AAY33766 standard; protein; 495 AA.
DE hKv5.1 human brain-specific potassium channel.
PN WO9941372-A1.
PD 19-AUG-1999.
PA (ZENE) ZENECA LTD.

RESULT 982
Query Match
Best Local Similarity 6.1%; 23.2%;
Score 73; DB 2; Length 501; Pred. No. 45;
ID AB063300 standard; protein; 501 AA.
DE Klebsiella pneumoniae polypeptide seqid 9817.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.

RESULT 983
Query Match
Best Local Similarity 6.1%; 26.5%;
Score 73; DB 7; Length 526; Pred. No. 46;
ID ABP53583 standard; protein; 526 AA.
DE Human NOV13b protein SEQ ID NO:30.
PN WO2002062999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.

RESULT 984
Query Match
Best Local Similarity 6.1%; 23.3%;
Score 73; DB 5; Length 526; Pred. No. 49;
ID ADH42229 standard; protein; 526 AA.
DE Novel human protein NOV50d.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.

RESULT 985
Query Match
Best Local Similarity 6.1%; 23.3%;
Score 73; DB 6; Length 553; Pred. No. 49;
ID ABU31136 standard; protein; 553 AA.
DE Protein encoded by Prokaryotic essential gene #16663.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (CURA-) CURAGEN CORP.

RESULT 986
Query Match
Best Local Similarity 6.1%; 19.6%;
Score 73; DB 3; Length 556; Pred. No. 53;
ID AAG24011 standard; protein; 556 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27526.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (ELIT-) ELITRA PHARM INC.

RESULT 987
Query Match
Best Local Similarity 6.1%; 22.0%;
Score 73; DB 8; Length 608; Pred. No. 53;
ID ADQ96000 standard; protein; 608 AA.
DE T cell activation associated protein #89.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAHI KASEI PHARMA CORP.

RESULT 988
Query Match
Best Local Similarity 6.1%; 19.5%;
Score 73; DB 8; Length 635; Pred. No. 60;
ID ADR99134 standard; protein; 635 AA.
DE Human protein similar to yeast SSM4, TEB4, SEQ ID 140.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.

RESULT 989
Query Match
Best Local Similarity 6.1%; 19.5%;
Score 73; DB 4; Length 717; Pred. No. 64;
ID ABB71311 standard; protein; 717 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40725.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.

RESULT 990
Query Match
Best Local Similarity 6.1%; 21.3%;
Score 73; DB 2; Length 746; Pred. No. 76;
ID AAW26673 standard; protein; 746 AA.
DE Staphylococcus aureus spoIIIE protein.
PN WO9726338-A1.
PD 24-JUL-1997.
PA (SMIK) SMITHKLINE BEECHAM PLC.

RESULT 991
Query Match
Best Local Similarity 6.1%; 23.3%;
Score 73; DB 4; Length 748; Pred. No. 80;
ID AAU37199 standard; protein; 748 AA.
DE Staphylococcus aureus cellular proliferation protein #1369.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.

RESULT 992
ID   AAW88407 standard; protein; 750 AA.
DE   Human adult neural tissue secreted protein s195_10.
PN   WO9857976-A1.
PD   23-DEC-1998.
PA   (GEMY/) GENETICS INST INC.
Query Match   19.5%; Score 73; DB 2; Length 750;
Best Local Similarity   19.5%; Pred. No. 80;

RESULT 993
ID   AED72894 standard; protein; 750 AA.
DE   Human clone s195_10 encoding cDNA SEQ ID NO:86.
PN   US2005250180-A1.
PD   10-NOV-2005.
PA   (JACO/) JACOBS K.
PA   (MCCO/) MCCOY J M.
PA   (LAVA/) LAVALLIE E R.
PA   (COLL/) COLLINS-RACIE L A.
PA   (EVAN/) EVANS C.
PA   (MERB/) MERBERG D.
PA   (TREA/) TREACY M.
PA   (SPAU/) SPAULDING V.
Query Match   19.5%; Score 73; DB 9; Length 750;
Best Local Similarity   19.5%; Pred. No. 80;

RESULT 994
ID   AAW26672 standard; protein; 788 AA.
DE   Staphylococcus aureus spoIIIE protein.
PN   WO9726338-A1.
PD   24-JUL-1997.
PA   (SMIK) SMITHKLINE BEECHAM PLC.
Query Match   23.3%; Score 73; DB 2; Length 788;
Best Local Similarity   23.3%; Pred. No. 86;

RESULT 995
ID   ABU42392 standard; protein; 788 AA.
DE   Protein encoded by Prokaryotic essential gene #27919.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   23.3%; Score 73; DB 6; Length 788;
Best Local Similarity   23.3%; Pred. No. 86;

RESULT 996
ID   AAU36734 standard; protein; 792 AA.
DE   Staphylococcus aureus cellular proliferation protein #904.
PN   WO200170955-A2.
PD   27-SEP-2001.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   23.3%; Score 73; DB 4; Length 792;
Best Local Similarity   23.3%; Pred. No. 87;

RESULT 997
ID   ABJ19057 standard; protein; 792 AA.
DE   Pathogen specific antigen related staphylococcal protein SEQ ID No 334.
PN   WO200259148-A2.
PD   01-AUG-2002.
PA   (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
Query Match   23.3%; Score 73; DB 6; Length 792;
Best Local Similarity   23.3%; Pred. No. 87;

RESULT 998
ID   ABM73117 standard; protein; 792 AA.
DE   Staphylococcus aureus protein #2357.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
Query Match   23.3%; Score 73; DB 6; Length 792;
Best Local Similarity   23.3%; Pred. No. 87;

RESULT 999
ID   AAW60466 standard; protein; 845 AA.
DE   Protein encoded by fragment #6 isolated from Hepatitis C virus genome.
PN   WO9825960-A1.
PD   18-JUN-1998.
PA   (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
Query Match   26.2%; Score 73; DB 2; Length 845;
Best Local Similarity   26.2%; Pred. No. 95;

RESULT 1000
ID   ADQ95946 standard; protein; 910 AA.

DE   T cell activation associated protein #62.
PN   WO2000058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match   19.5%; Score 73; DB 8; Length 910;
Best Local Similarity   19.5%; Pred. No. 1.1e+02;

RESULT 1001
ID   ABG24246 standard; protein; 913 AA.
DE   Novel human diagnostic protein #24237.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Query Match   19.5%; Score 73; DB 8; Length 913;
Best Local Similarity   19.5%; Pred. No. 1.1e+02;

RESULT 1002
ID   AAM51861 standard; protein; 966 AA.
DE   Murine polycystic kidney disease protein 2.
PN   US2002035056-A1.
PD   21-MAR-2002.
PA   (CURT/) CURTIS R A J.
PA   (SILO/) SILOS-SANTIAGO I.
Query Match   21.3%; Score 73; DB 5; Length 966;
Best Local Similarity   21.3%; Pred. No. 1.1e+02;

RESULT 1003
ID   ABB07819 standard; protein; 966 AA.
DE   Mouse polycystic kidney disease protein 2.
PN   US2002035056-A1.
PD   21-MAR-2002.
PA   (GENO-) GENOX RES INC.
Query Match   21.3%; Score 73; DB 5; Length 966;
Best Local Similarity   21.3%; Pred. No. 1.1e+02;

RESULT 1004
ID   ADJ76159 standard; protein; 966 AA.
DE   Marker gene related amino acid sequence SEQ ID NO:1411.
PN   EP1394274-A2.
PD   03-MAR-2004.
PA   (MILL-) MILLENIUM PHARM INC.
Query Match   21.3%; Score 73; DB 5; Length 966;
Best Local Similarity   21.3%; Pred. No. 1.1e+02;

RESULT 1005
ID   ADV66235 standard; protein; 966 AA.
DE   Polycystic kidney disease protein 2, SEQ ID 11.
PN   US2004248160-A1.
PD   09-DEC-2004.
PA   (MILL-) MILLENNIUM PHARM INC.
Query Match   21.3%; Score 73; DB 9; Length 966;
Best Local Similarity   21.3%; Pred. No. 1.1e+02;

RESULT 1006
ID   ADZ26335 standard; protein; 966 AA.
DE   Human hypoxia-responsive protein CNGH0002.1.
PN   WO2005033293-A2.
PD   14-APR-2005.
PA   (CENZ) CENTOCOR INC.
Query Match   19.5%; Score 73; DB 9; Length 966;
Best Local Similarity   19.5%; Pred. No. 1.1e+02;

RESULT 1007
ID   ABG05866 standard; protein; 971 AA.
DE   Novel human diagnostic protein #5857.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Query Match   19.5%; Score 73; DB 8; Length 971;
Best Local Similarity   19.5%; Pred. No. 1.1e+02;

RESULT 1008
ID   ADR99135 standard; protein; 971 AA.
DE   Human protein similar to yeast SSM4, TEB4, SEQ ID 141.
PN   WO2004078035-A2.
PD   16-SEP-2004.
PA   (FARB) BAYER PHARM CORP.
Query Match   19.5%; Score 73; DB 8; Length 971;
Best Local Similarity   19.5%; Pred. No. 1.1e+02;

RESULT 1009
ID   ADZ11480 standard; protein; 971 AA.

DE   MARCH VI protein, SEQ ID 49.
PN   US20050079613-A1.
PD   14-APR-2005.
PA   (UYOR-) UNIV OREGON HEALTH SCI.
     Query Match   6.1%; Score 73; DB 9; Length 971;
     Best Local Similarity   19.5%; Pred. No. 1.1e+02;

RESULT 1010
ID   AD2I1490 standard; protein; 971 AA.
DE   MARCH VI protein, SEQ ID 59.
PN   US20050079613-A1.
PD   14-APR-2005.
PA   (UYOR-) UNIV OREGON HEALTH SCI.
     Query Match   6.1%; Score 73; DB 9; Length 971;
     Best Local Similarity   19.5%; Pred. No. 1.1e+02;

RESULT 1011
ID   ABG07373 standard; protein; 976 AA.
DE   Novel human diagnostic protein #7364.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   6.1%; Score 73; DB 4; Length 976;
     Best Local Similarity   19.5%; Pred. No. 1.2e+02;

RESULT 1012
ID   ADX40795 standard; protein; 3010 AA.
DE   HCV polymerase protein #18.
PN   WO200512502-A2.
PD   10-FEB-2005.
PA   (EPIM-) EPIMMUNE INC.
     Query Match   6.1%; Score 73; DB 9; Length 3010;
     Best Local Similarity   26.2%; Pred. No. 5.5e+02;

RESULT 1013
ID   ABU05456 standard; protein; 209 AA.
DE   M. tuberculosis and M. leprae marker protein #107.
PN   WO200274903-A2.
PD   26-SEP-2002.
PA   (INSP) INST PASTEUR.
     Query Match   6.1%; Score 73; DB 5; Length 209;
     Best Local Similarity   22.1%; Pred. No. 16;

RESULT 1014
ID   ABU15302 standard; protein; 222 AA.
DE   Protein encoded by Prokaryotic essential gene #829.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   6.1%; Score 72.5; DB 6; Length 222;
     Best Local Similarity   20.5%; Pred. No. 17;

RESULT 1015
ID   ADY24595 standard; protein; 274 AA.
DE   Plant full length insert polypeptide seqid 72379.
PN   US20040034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match   6.1%; Score 72.5; DB 8; Length 274;
     Best Local Similarity   26.5%; Pred. No. 23;

RESULT 1016
ID   ADX95386 standard; protein; 274 AA.
DE   Plant full length insert polypeptide seqid 58050.
PN   US20040034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match   6.1%; Score 72.5; DB 8; Length 274;
     Best Local Similarity   26.5%; Pred. No. 23;

RESULT 1017

ID   ABB53879 standard; protein; 307 AA.
DE   Lactococcus lactis protein yfgG.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG) INRA INST NAT RECH AGRONOMIQUE.
     Query Match   6.1%; Score 72.5; DB 5; Length 307;
     Best Local Similarity   22.9%; Pred. No. 27;

RESULT 1018
ID   ADY10668 standard; protein; 307 AA.
DE   Plant full length insert polypeptide seqid 66483.
PN   US20040034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match   6.1%; Score 72.5; DB 8; Length 307;
     Best Local Similarity   25.3%; Pred. No. 27;

RESULT 1019
ID   ADY11265 standard; protein; 307 AA.
DE   Plant full length insert polypeptide seqid 67080.
PN   US20040034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match   6.1%; Score 72.5; DB 8; Length 307;
     Best Local Similarity   25.3%; Pred. No. 27;

RESULT 1020
ID   ADY10993 standard; protein; 307 AA.
DE   Plant full length insert polypeptide seqid 66808.
PN   US20040034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match   6.1%; Score 72.5; DB 8; Length 307;
     Best Local Similarity   25.3%; Pred. No. 27;

RESULT 1021
ID   ADY11014 standard; protein; 308 AA.
DE   Plant full length insert polypeptide seqid 66829.
PN   US20040034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match   6.1%; Score 72.5; DB 8; Length 308;
     Best Local Similarity   25.3%; Pred. No. 27;

RESULT 1022
ID   ADY10930 standard; protein; 310 AA.
DE   Plant full length insert polypeptide seqid 66745.
PN   US20040034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match   6.1%; Score 72.5; DB 8; Length 310;
     Best Local Similarity   25.3%; Pred. No. 27;

RESULT 1023

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ID   ADY11546 standard; protein; 310 AA.
DE   Plant full length insert polypeptide seqid 67361.
PN   US20040348888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match
     Best Local Similarity   25.3%;  Score 72.5;  DB 8;  Length 310;

RESULT 1024
ID   ADY09462 standard; protein; 311 AA.
DE   Plant full length insert polypeptide seqid 65277.
PN   US20040348888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match
     Best Local Similarity   25.3%;  Score 72.5;  DB 8;  Length 311;

RESULT 1025
ID   ADY11115 standard; protein; 312 AA.
DE   Plant full length insert polypeptide seqid 66930.
PN   US20040348888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match
     Best Local Similarity   25.3%;  Score 72.5;  DB 8;  Length 312;

RESULT 1026
ID   ADY10946 standard; protein; 312 AA.
DE   Plant full length insert polypeptide seqid 66761.
PN   US20040348888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match
     Best Local Similarity   25.3%;  Score 72.5;  DB 8;  Length 312;

RESULT 1027
ID   ABB53675 standard; protein; 325 AA.
DE   Lactococcus lactis protein ydhB.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
     Query Match
     Best Local Similarity   25.9%;  Score 72.5;  DB 5;  Length 325;

RESULT 1028
ID   ADH87677 standard; protein; 353 AA.
DE   Enterococcus faecalis polypeptide #2157.
PN   US6617156-B1.
PD   09-SEP-2003.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.
     Query Match
     Best Local Similarity   21.5%;  Score 72.5;  DB 7;  Length 353;

RESULT 1029
ID   ADH87557 standard; protein; 359 AA.
DE   Enterococcus faecalis polypeptide #2037.
PN   US6617156-B1.
PD   09-SEP-2003.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.
     Query Match
     Best Local Similarity   25.0%;  Score 72.5;  DB 7;  Length 359;

RESULT 1030
ID   AAR37264 standard; protein; 389 AA.
DE   Oxytocin receptor.
PN   EP542424-A1.
PD   19-MAY-1993.
PA   (ROHT ) ROHTO PHARM CO LTD.
     Query Match
     Best Local Similarity   24.5%;  Score 72.5;  DB 2;  Length 389;

RESULT 1031
ID   AAW23832 standard; protein; 389 AA.
DE   Human oxytocin receptor.
PN   EP811684-A2.
PD   10-DEC-1997.
PA   (ROHT ) ROHTO PHARM CO LTD.
     Query Match
     Best Local Similarity   24.5%;  Score 72.5;  DB 2;  Length 389;

RESULT 1032
ID   AAM40217 standard; protein; 389 AA.
DE   Human polypeptide SEQ ID NO 3362.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match
     Best Local Similarity   24.5%;  Score 72.5;  DB 4;  Length 389;

RESULT 1033
ID   ABP81865 standard; protein; 389 AA.
DE   Human oxytocin receptor protein SEQ ID NO:215.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
     Query Match
     Best Local Similarity   24.5%;  Score 72.5;  DB 6;  Length 389;

RESULT 1034
ID   AAE38317 standard; protein; 389 AA.
DE   Human oxytocin receptor protein.
PN   WO2003064402-A1.
PD   07-AUG-2003.
PA   (PFIZ ) PFIZER LTD.
PA   (PFIZ ) PFIZER INC.
     Query Match
     Best Local Similarity   24.5%;  Score 72.5;  DB 6;  Length 389;

RESULT 1035
ID   ADP12125 standard; protein; 389 AA.
DE   Human oxytocin receptor (OXTR) protein SEQ ID NO:2.
PN   WO2003093816-A2.
PD   13-NOV-2003.
PA   (FARB ) BAYER AG.
     Query Match
     Best Local Similarity   24.5%;  Score 72.5;  DB 8;  Length 389;

RESULT 1036
ID   ADI03915 standard; protein; 389 AA.
DE   Human oxytocin receptor polypeptide.
PN   WO2004000993-A2.
PD   31-DEC-2003.
PA   (UYQU-) UNIV QUEBEC A MONTREAL.
PA   (UYMO-) UNIV MONTREAL CENT HOSPITALIER.
     Query Match
     Best Local Similarity   24.5%;  Score 72.5;  DB 8;  Length 389;

RESULT 1037
ID   ADO29590 standard; protein; 389 AA.
DE   Human GPCR OXTR, SEQ ID NO:692.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
     Query Match
     Best Local Similarity   24.5%;  Score 72.5;  DB 8;  Length 389;

RESULT 1038
ID   ADW98687 standard; protein; 389 AA.
DE   Human oxytocin receptor (OXTR) protein SeqID1.
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PN   WO2005012565-A1.
PD   10-FEB-2005.
PA   (ASTR ) ASTRAZENECA AB.
PA   (ASTR ) ASTRAZENECA UK LTD.

RESULT 1039
Query Match             24.5%;
Best Local Similarity   6.1%;  Score  72.5;  DB  9;  Pred. No.  37;  Length  389;
ID   AAR58665 standard; protein; 448 AA.
DE   Bovine PACAP receptor type 1B mature protein.
PN   EP618291-A2.
PD   05-OCT-1994.
PA   (TAKE ) TAKEDA CHEM IND LTD.

RESULT 1040
Query Match             29.6%;
Best Local Similarity   6.1%;  Score  72.5;  DB  2;  Pred. No.  45;  Length  448;
ID   AAR58663 standard; protein; 476 AA.
DE   Bovine PACAP receptor type 1A mature protein.
PN   EP618291-A2.
PD   05-OCT-1994.
PA   (TAKE ) TAKEDA CHEM IND LTD.

RESULT 1041
Query Match             29.6%;
Best Local Similarity   6.1%;  Score  72.5;  DB  2;  Pred. No.  49;  Length  476;
ID   AAR58657 standard; protein; 485 AA.
DE   Bovine PACAP receptor type 1B protein.
PN   EP618291-A2.
PD   05-OCT-1994.
PA   (TAKE ) TAKEDA CHEM IND LTD.

RESULT 1042
Query Match             29.6%;
Best Local Similarity   6.1%;  Score  72.5;  DB  2;  Pred. No.  50;  Length  485;
ID   AAR58655 standard; protein; 513 AA.
DE   Bovine PACAP receptor type 1A protein.
PN   EP618291-A2.
PD   05-OCT-1994.
PA   (TAKE ) TAKEDA CHEM IND LTD.

RESULT 1043
Query Match             29.6%;
Best Local Similarity   6.1%;  Score  72.5;  DB  2;  Pred. No.  54;  Length  513;
ID   ADN19765 standard; protein; 522 AA.
DE   Bacterial polypeptide #2418.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.

RESULT 1044
Query Match             22.5%;
Best Local Similarity   6.1%;  Score  72.5;  DB  8;  Pred. No.  56;  Length  522;
ID   ADV89115 standard; protein; 666 AA.
DE   Streptococcus agalactiae protein sequence, SEQ ID 1509.
PN   FR2824074-A1.
PD   31-OCT-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.

RESULT 1045
Query Match             23.1%;
Best Local Similarity   6.1%;  Score  72.5;  DB  8;  Pred. No.  78;  Length  666;
ID   ADV82479 standard; protein; 666 AA.
DE   Streptococcus agalactiae protein, SEQ ID 3620.
PN   WO2002092818-A2.
PD   21-NOV-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.

RESULT 1046
Query Match             23.1%;
Best Local Similarity   6.1%;  Score  72.5;  DB  8;  Pred. No.  78;  Length  666;
ID   ADV80368 standard; protein; 666 AA.
DE   Streptococcus agalactiae protein, SEQ ID 1509.
PN   WO2002092818-A2.
PD   21-NOV-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.

RESULT 1047
Query Match             23.1%;
Best Local Similarity   6.1%;  Score  72.5;  DB  8;  Pred. No.  78;  Length  666;
ID   ADI81620 standard; protein; 769 AA.
DE   C. elegans protein similar to Pfam PF00023.
PN   US20040099537-A1.
PD   15-JAN-2004.
PA   (ROOS/) ROOS J.
PA   (STAU/) STAUDERMAN K.
PA   (VELI/) VELICELEBI G.

RESULT 1048
Query Match             20.2%;
Best Local Similarity   6.1%;  Score  72.5;  DB  5;  Pred. No.  95;  Length  769;
ID   ABB05429 standard; protein; 848 AA.
DE   Arabidopsis thaliana ABH1 protein SEQ ID NO:2.
PN   WO200196585-A2.
PD   20-DEC-2001.
PA   (REGC ) UNIV CALIFORNIA.

RESULT 1049
Query Match             22.3%;
Best Local Similarity   6.1%;  Score  72.5;  DB  6;  Pred. No.  1.1e+02;  Length  848;
ID   AAB31528 standard; protein; 848 AA.
DE   Arabidopsis thaliana protein used to isolate rice CBP80 orthologues.
PN   WO200281696-A2.
PD   17-OCT-2002.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.

RESULT 1050
Query Match             22.3%;
Best Local Similarity   6.1%;  Score  72.5;  DB  6;  Pred. No.  1.1e+02;  Length  848;
ID   ABU25159 standard; protein; 851 AA.
DE   Protein encoded by Prokaryotic essential gene #10686.
PN   WO2002277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.

RESULT 1051
Query Match             20.5%;
Best Local Similarity   6.1%;  Score  72.5;  DB  6;  Pred. No.  1.1e+02;  Length  851;
ID   ADY10144 standard; protein; 903 AA.
DE   Plant full length insert polypeptide seqid 65959.
PN   US20040034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.

RESULT 1052
Query Match             18.1%;
Best Local Similarity   6.1%;  Score  72.5;  DB  8;  Pred. No.  1.2e+02;  Length  903;
ID   ADW76078 standard; protein; 1051 AA.
DE   Human cytomegalovirus (HCMV) pp65-IE1 fusion protein.
PN   WO2005007689-A1.
PD   27-JAN-2005.
PA   (ALPH-) ALPHAVAX INC.

RESULT 1053
Query Match             19.3%;
Best Local Similarity   6.1%;  Score  72.5;  DB  9;  Pred. No.  1.5e+02;  Length  1051;
ID   AAR34580 standard; protein; 3010 AA.
DE   Human hepatitis C virus gene encoded polypeptide.
PN   EP541089-A2.
PD   12-MAY-1993.
PA   (SANW ) SANWA KAGAKU KENKYUSHO CO.

RESULT 1054
Query Match             23.7%;
Best Local Similarity   6.1%;  Score  72.5;  DB  2;  Pred. No.  6.3e+02;  Length  3010;
ID   ADQ96378 standard; protein; 208 AA.
DE   T cell activation associated protein #278.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
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RESULT 1055
Query Match
Best Local Similarity 20.8%;   Score 72; DB 8; Length 208;
ID   AED36113 standard; protein; 260 AA.
DE   Tobacco NAP1-like protein (NtNAP1b).
PN   WO200509454562-A1.
PD   13-OCT-2005.
PA   (CROP-) CROPDESIGN NV.

RESULT 1056
Query Match   6.0%;
Best Local Similarity 31.6%;   Score 72; DB 9; Length 260;
ID   ABB48543 standard; protein; 306 AA.
DE   Listeria monocytogenes protein #1247.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP-) INST PASTEUR.

RESULT 1057
Query Match   6.0%;
Best Local Similarity 21.0%;   Score 72; DB 5; Length 306;
ID   ABU39432 standard; protein; 317 AA.
DE   Protein encoded by Prokaryotic essential gene #24959.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.

RESULT 1058
Query Match   6.0%;
Best Local Similarity 23.5%;   Score 72; DB 3; Length 317;
ID   AAB53392 standard; protein; 334 AA.
DE   Human colon cancer antigen protein sequence SEQ ID NO:932.
PN   WO200055351-A1.
PD   21-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.

RESULT 1059
Query Match   6.0%;
Best Local Similarity 28.8%;   Score 72; DB 3; Length 334;
ID   AAY97505 standard; protein; 370 AA.
DE   Human G coupled-protein receptor, hGR3.
PN   WO200017641-A1.
PD   30-MAR-2000.
PA   (MILL-) MILLENNIUM PHARM INC.

RESULT 1060
Query Match   6.0%;
Best Local Similarity 21.8%;   Score 72; DB 3; Length 370;
ID   AAW20731 standard; protein; 375 AA.
DE   H. Pylori inner membrane protein, 06cp111l8orf6.
PN   WO9640893-A1.
PD   19-DEC-1996.
PA   (ASTR-) ASTRA AB.

RESULT 1061
Query Match   6.0%;
Best Local Similarity 20.9%;   Score 72; DB 2; Length 375;
ID   ABU19932 standard; protein; 396 AA.
DE   Protein encoded by Prokaryotic essential gene #5459.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.

RESULT 1062
Query Match   6.0%;
Best Local Similarity 21.6%;   Score 72; DB 6; Length 396;
ID   ABG25051 standard; protein; 414 AA.
DE   Novel human diagnostic protein #25042.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSB-) HYSEQ INC.

RESULT 1063
Query Match   6.0%;
Best Local Similarity 22.6%;   Score 72; DB 4; Length 414;
ID   AAG50203 standard; protein; 427 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 63592.
PN   EP1033405-A2.
PD   06-SEP-2000.
PA
Query Match   6.0%;
Best Local Similarity 22.0%;   Score 72; DB 3; Length 427;

RESULT 1064
ID   AAG50202 standard; protein; 430 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 63591.
PN   EP1033405-A2.
PD   06-SEP-2000.
Query Match
Best Local Similarity 22.0%;   Score 72; DB 3; Length 430;

RESULT 1065
ID   ABM72825 standard; protein; 447 AA.
DE   Staphylococcus aureus protein #2065.
PN   WO200294868-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
RESULT 1066
Query Match   6.0%;
Best Local Similarity 22.0%;   Score 72; DB 6; Length 447;
ID   ABB62902 standard; protein; 448 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 15498.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE-) PE CORP NY.
RESULT 1067
Query Match   6.0%;
Best Local Similarity 23.9%;   Score 72; DB 4; Length 448;
ID   ABU18913 standard; protein; 453 AA.
DE   Pathogen specific antigen related staphylococcal protein SEQ ID NO 59.
PN   WO200259148-A2.
PD   01-AUG-2002.
PA   (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
RESULT 1068
Query Match   6.0%;
Best Local Similarity 25.1%;   Score 72; DB 6; Length 453;
ID   ABU16441 standard; protein; 453 AA.
DE   Protein encoded by Prokaryotic essential gene #1968.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
RESULT 1069
Query Match   6.0%;
Best Local Similarity 23.9%;   Score 72; DB 6; Length 453;
ID   ADN73057 standard; protein; 468 AA.
DE   Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 952.
PN   WO2004035798-A2.
PD   29-APR-2004.
PA   (CROP-) CROPDESIGN NV.
RESULT 1070
Query Match   6.0%;
Best Local Similarity 23.9%;   Score 72; DB 8; Length 468;
ID   AAG16338 standard; protein; 495 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 16945.
PN   EP1033405-A2.
PD   06-SEP-2000.
RESULT 1071
Query Match   6.0%;
Best Local Similarity 21.8%;   Score 72; DB 3; Length 495;
ID   AAG16337 standard; protein; 497 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 16944.
PN   EP1033405-A2.
PD   06-SEP-2000.
RESULT 1072
Query Match   6.0%;
Best Local Similarity 21.3%;   Score 72; DB 3; Length 497;
ID   AED61108 standard; protein; 497 AA.
DE   Thale cress protein #81.
PN   US200524678S-A1.
PD   03-NOV-2005.
PA   (CERE-) CERES INC.
RESULT 1073
Query Match   6.0%;
Best Local Similarity 21.3%;   Score 72; DB 9; Length 497;
ID   AEF26566 standard; protein; 497 AA.
DE   A. thaliana cytochrome P450 homolog SEQ ID NO: 85.
PN   US20060015970-A1.

PD   19-JAN-2006.
PA   (CERS-) CERS INC.
     Query Match   6.0%; Score 72; DB 10; Length 497;
     Best Local Similarity   21.3%; Pred. No. 60;
RESULT 1074
ID   AAG16336 standard; protein; 507 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 16943.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   6.0%; Score 72; DB 3; Length 507;
     Best Local Similarity   21.3%; Pred. No. 61;
RESULT 1075
ID   ADS23568 standard; protein; 543 AA.
DE   Bacterial polypeptide #12601.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (GOLD/) GOLDMAN B S.
PA   (CHEN/) CHEN X.
PA   (SLAT/) SLATER S C.
PA   (HINK/) HINKLE G J.
PA   (CAOY/) CAO Y.
     Query Match   6.0%; Score 72; DB 8; Length 543;
     Best Local Similarity   18.6%; Pred. No. 67;
RESULT 1076
ID   ABU25738 standard; protein; 552 AA.
DE   Protein encoded by Prokaryotic essential gene #11265.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   6.0%; Score 72; DB 6; Length 552;
     Best Local Similarity   19.5%; Pred. No. 69;
RESULT 1077
ID   AAG50201 standard; protein; 556 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 63590.
PN   EP1033405-A2.
PD   06-SEP-2000.
     Query Match   6.0%; Score 72; DB 3; Length 556;
     Best Local Similarity   22.0%; Pred. No. 70;
RESULT 1078
ID   ADJ69383 standard; protein; 594 AA.
DE   Human heat mitochondrial protein as a therapeutic target SeqID1189.
PN   WO200308768-A2.
PD   23-OCT-2003.
PA   (MITO-) MITOKOR.
     Query Match   6.0%; Score 72; DB 7; Length 594;
     Best Local Similarity   20.8%; Pred. No. 76;
RESULT 1079
ID   ABP97202 standard; protein; 696 AA.
DE   Tumour-associated antigenic target protein TAT247 SEQ ID NO:84.
PN   WO200324392-A2.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   6.0%; Score 72; DB 6; Length 696;
     Best Local Similarity   20.8%; Pred. No. 95;
RESULT 1080
ID   ABP97201 standard; protein; 696 AA.
DE   Tumour-associated antigenic target protein TAT225 SEQ ID NO:83.
PN   WO200324392-A2.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   6.0%; Score 72; DB 6; Length 696;
     Best Local Similarity   20.8%; Pred. No. 95;
RESULT 1081
ID   ABP81969 standard; protein; 696 AA.
DE   Human GPCR XPR1 protein SEQ ID NO:424.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
     Query Match   6.0%; Score 72; DB 6; Length 696;
     Best Local Similarity   20.8%; Pred. No. 95;
RESULT 1082
ID   ADB67652 standard; protein; 696 AA.

DE   Human xenotropic& polytropic retrovirus receptor, SEQ ID 21.
PN   WO2003072824-A1.
PD   04-SEP-2003.
PA   (SANY) SANKYO CO LTD.
     Query Match   6.0%; Score 72; DB 7; Length 696;
     Best Local Similarity   20.8%; Pred. No. 95;
RESULT 1083
ID   ADQ96380 standard; protein; 696 AA.
DE   T cell activation associated protein #279.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
     Query Match   6.0%; Score 72; DB 8; Length 696;
     Best Local Similarity   21.3%; Pred. No. 95;
RESULT 1084
ID   ABM69179 standard; protein; 724 AA.
DE   Photorhabdus luminescens protein sequence #2276.
PN   WO200294867-A2.
PD   28-NOV-2002.
PA   (INSP) INST PASTEUR.
PA   (CNRS) CNRS CENT NAT RECH SCI.
     Query Match   6.0%; Score 72; DB 6; Length 724;
     Best Local Similarity   21.3%; Pred. No. 1e+02;
RESULT 1085
ID   AAB46702 standard; protein; 741 AA.
DE   P. falciparum DNA polymerase protein fragment SEQ ID NO 11.
PN   WO200075335-A2.
PD   14-DEC-2000.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match   6.0%; Score 72; DB 4; Length 741;
     Best Local Similarity   30.4%; Pred. No. 1e+02;
RESULT 1086
ID   AAM47977 standard; protein; 788 AA.
DE   Human hARRG.
PN   CN1315342-A.
PD   03-OCT-2001.
PA   (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
     Query Match   6.0%; Score 72; DB 5; Length 788;
     Best Local Similarity   26.3%; Pred. No. 1.1e+02;
RESULT 1087
ID   ABB58917 standard; protein; 1275 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 3543.
PN   WO20017I042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   6.0%; Score 72; DB 4; Length 1275;
     Best Local Similarity   19.0%; Pred. No. 2.2e+02;
RESULT 1088
ID   AAY70064 standard; protein; 2307 AA.
DE   Recombinant fusion pHCAP-1 polyprotein.
PN   WO20008469-A1.
PD   17-FEB-2000.
PA   (AGOU-) AGOURON PHARM INC.
     Query Match   6.0%; Score 72; DB 3; Length 2307;
     Best Local Similarity   23.6%; Pred. No. 5e+02;
RESULT 1089
ID   AAY70065 standard; protein; 2307 AA.
DE   Recombinant fusion pHCAP-3 polyprotein.
PN   WO20008469-A1.
PD   17-FEB-2000.
PA   (AGOU-) AGOURON PHARM INC.
     Query Match   6.0%; Score 72; DB 3; Length 2307;
     Best Local Similarity   23.6%; Pred. No. 5e+02;
RESULT 1090
ID   AAY70066 standard; protein; 2307 AA.
DE   Recombinant fusion pHCAP-4 polyprotein.
PN   WO20008469-A1.
PD   17-FEB-2000.
PA   (AGOU-) AGOURON PHARM INC.
     Query Match   6.0%; Score 72; DB 3; Length 2307;
     Best Local Similarity   23.6%; Pred. No. 5e+02;
RESULT 1091
ID   AAM93791 standard; protein; 208 AA.

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DE   Human polypeptide, SEQ ID NO: 3817.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.
  Query Match
  Best Local Similarity   25.2%;   Score 71.5;   DB 4;   Length 208;

RESULT 1092
ID   ADL31784 standard; protein; 208 AA.
DE   Human protein encoded by a full length cDNA clone SeqID 3817.
PN   EP1136543-A2.
PD   10-MAR-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
  Query Match
  Best Local Similarity   25.2%;   Score 71.5;   DB 8;   Length 208;

RESULT 1093
ID   AAG56417 standard; protein; 209 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 72517.
PN   EP1033405-A2.
PD   06-SEP-2000.
  Query Match
  Best Local Similarity   25.6%;   Score 71.5;   DB 3;   Length 209;

RESULT 1094
ID   AAG56416 standard; protein; 216 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 72516.
PN   EP1033405-A2.
PD   06-SEP-2000.
  Query Match
  Best Local Similarity   25.6%;   Score 71.5;   DB 3;   Length 216;

RESULT 1095
ID   AAG16922 standard; protein; 218 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 17750.
PN   EP1033405-A2.
PD   06-SEP-2000.
  Query Match
  Best Local Similarity   42.4%;   Score 71.5;   DB 3;   Length 218;

RESULT 1096
ID   ABB53486 standard; protein; 301 AA.
DE   Lactococcus lactis protein ybiG.
PN   FR2870446-A1.
PD   12-OCT-2001.
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
  Query Match
  Best Local Similarity   26.5%;   Score 71.5;   DB 5;   Length 301;

RESULT 1097
ID   AAW37976 standard; protein; 342 AA.
DE   Kaposi's sarcoma associated herpesvirus G protein-coupled receptor.
PN   WO9815289-A1.
PD   16-APR-1998.
PA   (CORR ) CORNELL RES FOUND INC.
  Query Match
  Best Local Similarity   22.2%;   Score 71.5;   DB 2;   Length 342;

RESULT 1098
ID   ADG87423 standard; protein; 348 AA.
DE   Meloidogyne incognita plk1 protein.
PN   US2003150017-A1.
PD   07-AUG-2003.
PA   (MESA-) MESA J R B.
PA   (GRAH/) GRAHAM M W.
PA   (FAIR/) FAIRBAIRN D J.
  Query Match
  Best Local Similarity   21.0%;   Score 71.5;   DB 7;   Length 348;

RESULT 1099
ID   AEF77681 standard; protein; 362 AA.
DE   Rat prostaglandin E receptor 2 (PTGER2).
PN   WO2006017171-A2.
PD   16-FEB-2006.
PA   (META-) METABOLEX INC.
  Query Match
  Best Local Similarity   24.2%;   Score 71.5;   DB 10;   Length 362;

RESULT 1100
ID   ADR40542 standard; protein; 363 AA.
DE   Ovine MLIA protein.
PN   US2004161823-A1.
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PD   19-AUG-2004.
PA   (FEDE/) FEDER J N.
PA   (MINT/) MINTIER G.
PA   (RAMA/) RAMANATHAN C S.
PA   (HAWK/) HAWKEN D R.
  Query Match
  Best Local Similarity   23.1%;   Score 71.5;   DB 8;   Length 363;

RESULT 1101
ID   AAR88410 standard; protein; 366 AA.
DE   High-affinity melatonin-1a receptor.
PN   WO9535320-A1.
PD   28-DEC-1995.
PA   (MASS-) MASSACHUSETTS GEN HOSPITAL.
  Query Match
  Best Local Similarity   23.1%;   Score 71.5;   DB 2;   Length 366;

RESULT 1102
ID   ABU00456 standard; protein; 382 AA.
DE   Angiogenesis-associated human protein sequence #1.
PN   WO200279492-A2.
PD   10-OCT-2002.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
  Query Match
  Best Local Similarity   22.3%;   Score 71.5;   DB 6;   Length 382;

RESULT 1103
ID   ABP58069 standard; protein; 382 AA.
DE   Human G-protein coupled receptor GAVE1.
PN   WO2002095056-A2.
PD   28-NOV-2002.
PA   (AVET ) AVENTIS PHARM INC.
  Query Match
  Best Local Similarity   22.3%;   Score 71.5;   DB 6;   Length 382;

RESULT 1104
ID   ABP59277 standard; protein; 382 AA.
DE   Human Edg1 receptor.
PN   WO2003006503-A1.
PD   23-JAN-2003.
PA   (CERE-) CERETEK.
  Query Match
  Best Local Similarity   22.3%;   Score 71.5;   DB 6;   Length 382;

RESULT 1105
ID   ABU08809 standard; protein; 382 AA.
DE   Human EDG-1 protein.
PN   US2002155512-A1.
PD   24-OCT-2002.
PA   (RIGE-) RIGEL PHARM INC.
  Query Match
  Best Local Similarity   22.3%;   Score 71.5;   DB 6;   Length 382;

RESULT 1106
ID   ABR59701 standard; protein; 382 AA.
DE   Human endothelial differentiation sphingolipid GPCR 1.
PN   WO2003029277-A2.
PD   10-APR-2003.
PA   (RIGE-) RIGEL PHARM INC.
  Query Match
  Best Local Similarity   22.3%;   Score 71.5;   DB 6;   Length 382;

RESULT 1107
ID   ABP81876 standard; protein; 382 AA.
DE   Human sphingolipid receptor Edg1 protein SEQ ID NO:237.
PN   WO2002061087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
  Query Match
  Best Local Similarity   22.3%;   Score 71.5;   DB 6;   Length 382;

RESULT 1108
ID   ADB67662 standard; protein; 382 AA.
DE   Human EDG1, SEQ ID 31.
PN   WO2003072824-A1.
PD   04-SEP-2003.
PA   (SANY ) SANKYO CO LTD.
  Query Match
  Best Local Similarity   22.3%;   Score 71.5;   DB 7;   Length 382;

RESULT 1109
ID   ADC40477 standard; protein; 382 AA.
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DE   Protein of human EDG-1.
PN   WO2003052096-A1.
PD   26-JUN-2003.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match
     Best Local Similarity   22.3%;   Score 71.5;   DB 7;   Pred. No. 47;   Length 382;

RESULT 1110
ID   ADN38684 standard; protein; 382 AA.
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:2.
PN   WO2003042661-A2.
PD   22-MAY-2003.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
     Query Match
     Best Local Similarity   22.3%;   Score 71.5;   DB 7;   Pred. No. 47;   Length 382;

RESULT 1111
ID   ABM85457 standard; protein; 382 AA.
DE   Human protein sequence hCP1630135.
PN   WO2003073826-A2.
PD   12-SEP-2003.
PA   (SAGR-) SAGRES DISCOVERY.
     Query Match
     Best Local Similarity   22.3%;   Score 71.5;   DB 7;   Pred. No. 47;   Length 382;

RESULT 1112
ID   ADJ45541 standard; protein; 382 AA.
DE   LXR-ligand induced transcript seq id 72.
PN   US20040023276-A1.
PD   05-FEB-2004.
PA   (WARD/) WARD T R.
PA   (MAOM/) MAO M.
PA   (LINS/) LINSLEY P S.
PA   (LUND/) LUND E.
     Query Match
     Best Local Similarity   22.3%;   Score 71.5;   DB 8;   Pred. No. 47;   Length 382;

RESULT 1113
ID   ADR67022 standard; protein; 382 AA.
DE   Human cancer associated protein sequence SEQ ID NO:68.
PN   WO2004074321-A2.
PD   02-SEP-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
     Query Match
     Best Local Similarity   22.3%;   Score 71.5;   DB 8;   Pred. No. 47;   Length 382;

RESULT 1114
ID   ADY19566 standard; protein; 382 AA.
DE   PRO polypeptide SEQ ID NO 5372.
PN   WO2005016962-A2.
PD   24-FEB-2005.
PA   (GETH ) GENENTECH INC.
     Query Match
     Best Local Similarity   22.3%;   Score 71.5;   DB 9;   Pred. No. 47;   Length 382;

RESULT 1115
ID   ADZ12975 standard; protein; 382 AA.
DE   Human cancer-associated protein #147.
PN   WO2005031001-A2.
PD   07-APR-2005.
PA   (CHIR ) CHIRON CORP.
     Query Match
     Best Local Similarity   22.3%;   Score 71.5;   DB 9;   Pred. No. 47;   Length 382;

RESULT 1116
ID   ADZ12973 standard; protein; 382 AA.
DE   Human cancer-associated protein #146.
PN   WO2005031001-A2.
PD   07-APR-2005.
PA   (CHIR ) CHIRON CORP.
     Query Match
     Best Local Similarity   22.3%;   Score 71.5;   DB 9;   Pred. No. 47;   Length 382;

RESULT 1117
ID   ADN19614 standard; protein; 383 AA.
DE   Bacterial polypeptide #2267.
PN   US20030233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (FARB ) BAYER AG.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match
     Best Local Similarity   22.0%;   Score 71.5;   DB 8;   Pred. No. 48;   Length 383;

RESULT 1118
ID   ABB05226 standard; protein; 390 AA.
DE   Catostomus commersoni isotocin receptor protein SEQ ID NO:3.
PN   WO200192296-A2.
PD   06-DEC-2001.
PA   (INCY-) INCYTE CORP.
     Query Match
     Best Local Similarity   22.2%;   Score 71.5;   DB 5;   Pred. No. 49;   Length 390;

RESULT 1119
ID   ADM83141 standard; protein; 394 AA.
DE   Rat vesicle membrane protein (VMP)2.
PN   WO200317335-A2.
PD   18-OCT-2002.
PA   (INCY-) INCYTE CORP.
     Query Match
     Best Local Similarity   22.7%;   Score 71.5;   DB 5;   Pred. No. 49;   Length 394;

RESULT 1120
ID   ABB48023 standard; protein; 435 AA.
DE   Listeria monocytogenes protein #727.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP-) INST PASTEUR.
     Query Match
     Best Local Similarity   21.4%;   Score 71.5;   DB 5;   Pred. No. 57;   Length 435;

RESULT 1121
ID   AAR22000 standard; protein; 441 AA.
DE   Partial M17 antigen from Region II, encoded by PCR prod.
PN   WO9203457-A.
PD   05-MAR-1992.
PA   (REGC ) UNIV CALIFORNIA.
     Query Match
     Best Local Similarity   22.6%;   Score 71.5;   DB 2;   Pred. No. 58;   Length 441;

RESULT 1122
ID   ADX93096 standard; protein; 448 AA.
DE   Plant full length insert polypeptide seqid 55760.
PN   US20040348888-A1.
PD   19-FEB-2004.
PA   (INCY-) INCYTE GENOMICS INC.
PA   (ZHOU/) ZHOU Y.
PA   (LIUJ/) LIU J.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match
     Best Local Similarity   22.3%;   Score 71.5;   DB 6;   Pred. No. 59;   Length 448;

RESULT 1123
ID   ABP75877 standard; protein; 470 AA.
DE   Human secretory polypeptide SPTM SEQ ID NO 1061.
PN   WO200283876-A2.
PD   24-OCT-2002.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match
     Best Local Similarity   22.4%;   Score 71.5;   DB 6;   Pred. No. 63;   Length 470;

RESULT 1124
ID   ABU26033 standard; protein; 524 AA.
DE   Protein encoded by Prokaryotic essential gene #115560.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match
     Best Local Similarity   22.3%;   Score 71.5;   DB 6;   Pred. No. 73;   Length 524;

RESULT 1125
ID   ABJ37074 standard; protein; 565 AA.
DE   Human breast cancer / ovarian cancer related protein #50.
PN   WO200300012-A2.
PD   03-JAN-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match
     Best Local Similarity   22.4%;   Score 71.5;   DB 6;   Pred. No. 81;   Length 565;
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RESULT 1126
ID   AAW51244 standard; protein; 568 AA.
DE   Human calcitonin receptor.
PN   WO9821242-A1.
PD   22-MAY-1998.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   6.0%;
     Best Local Similarity   22.4%;
     Score 71.5; DB 2; Length 568;

RESULT 1127
ID   ABU16392 standard; protein; 603 AA.
DE   Protein encoded by Prokaryotic essential gene #1919.
PN   WO20027183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match   6.0%;
     Best Local Similarity   21.3%;
     Score 71.5; DB 6; Length 603;

RESULT 1128
ID   ABM72619 standard; protein; 603 AA.
DE   Staphylococcus aureus protein #1859.
PN   WO20029468-A2.
PD   28-NOV-2002.
PA   (CHIR-) CHIRON SPA.
     Query Match   6.0%;
     Best Local Similarity   21.3%;
     Score 71.5; DB 6; Length 603;

RESULT 1129
ID   AEC46140 standard; protein; 689 AA.
DE   Human methionine synthase reductase (MTRR) mutant protein, SEQ ID NO: 48.
PN   US20051917101-A1.
PD   01-SEP-2005.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match   6.0%;
     Best Local Similarity   22.8%;
     Score 71.5; DB 9; Length 689;

RESULT 1130
ID   ADM43215 standard; protein; 697 AA.
DE   Human methionine synthase reductase del Arg 559 variant.
PN   US20030082676-A1.
PD   01-MAY-2003.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match   6.0%;
     Best Local Similarity   22.8%;
     Score 71.5; DB 7; Length 697;

RESULT 1131
ID   ADM43217 standard; protein; 697 AA.
DE   Human methionine synthase reductase del Leu 576 variant.
PN   US20030082676-A1.
PD   01-MAY-2003.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match   6.0%;
     Best Local Similarity   22.8%;
     Score 71.5; DB 7; Length 697;

RESULT 1132
ID   AEC46138 standard; protein; 697 AA.
DE   Human methionine synthase reductase (MTRR) mutant protein, SEQ ID NO: 46.
PN   US20051917101-A1.
PD   01-SEP-2005.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match   6.0%;
     Best Local Similarity   22.8%;
     Score 71.5; DB 9; Length 697;

RESULT 1133
ID   AAB07591 standard; protein; 698 AA.
DE   A human methionine synthase reductase polypeptide.
PN   WO200042196-A2.
PD   20-JUL-2000.
PA   (UYMC-) UNIV MCGILL.
     Query Match   6.0%;
     Best Local Similarity   22.8%;
     Score 71.5; DB 3; Length 698;

RESULT 1134
ID   ABG00883 standard; protein; 698 AA.
DE   Novel human diagnostic protein #874.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   6.0%;
     Best Local Similarity   22.8%;
     Score 71.5; DB 4; Length 698;

RESULT 1135
ID   ADM43211 standard; protein; 698 AA.
DE   Human methionine synthase reductase Met22Ile variant.
PN   US20030082676-A1.
PD   01-MAY-2003.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match   6.0%;
     Best Local Similarity   22.8%;
     Score 71.5; DB 7; Length 698;

RESULT 1136
ID   ADM43213 standard; protein; 698 AA.
DE   Human methionine synthase reductase Cys37Tyr variant.
PN   US20030082676-A1.
PD   01-MAY-2003.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match   6.0%;
     Best Local Similarity   22.8%;
     Score 71.5; DB 7; Length 698;

RESULT 1137
ID   ADM43207 standard; protein; 698 AA.
DE   Human wild-type methionine synthase reductase.
PN   US20030082676-A1.
PD   01-MAY-2003.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match   6.0%;
     Best Local Similarity   22.8%;
     Score 71.5; DB 7; Length 698;

RESULT 1138
ID   ADQ39857 standard; protein; 698 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1520.
PN   WO200405852-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
     Query Match   6.0%;
     Best Local Similarity   22.8%;
     Score 71.5; DB 8; Length 698;

RESULT 1139
ID   AEC46136 standard; protein; 698 AA.
DE   Human methionine synthase reductase (MTRR) mutant protein, SEQ ID NO: 44.
PN   US20051917101-A1.
PD   01-SEP-2005.
PA   (GRAV/) GRAVEL R A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
     Query Match   6.0%;
     Best Local Similarity   22.8%;
     Score 71.5; DB 9; Length 698;

RESULT 1140
ID   AEC46113 standard; protein; 698 AA.

DE   Human methionine synthase reductase (MTRR) protein, SEQ ID NO: 21.
PN   US20051917O1-A1.
PD   01-SEP-2005.
PA   (GRAV/) GRAVEL R. A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
Query Match
Best Local Similarity 22.8%;   Score 71.5;   DB 9;   Pred. No. 1.1e+02;   Length 698;

RESULT 1141
ID   AEC46134 standard; protein; 698 AA.
PN   US20051917O1-A1.
PD   01-SEP-2005.
DE   Human methionine synthase reductase (MTRR) mutant protein, SEQ ID NO: 42.
PN   US20051917O1-A1.
PD   01-SEP-2005.
PA   (GRAV/) GRAVEL R. A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
Query Match
Best Local Similarity 22.8%;   Score 71.5;   DB 9;   Pred. No. 1.1e+02;   Length 698;

RESULT 1142
ID   AEC46094 standard; protein; 698 AA.
DE   Human methionine synthase reductase (MTRR) protein, SEQ ID NO: 2.
PN   US20051917O1-A1.
PD   01-SEP-2005.
PA   (GRAV/) GRAVEL R. A.
PA   (ROZE/) ROZEN R.
PA   (LECL/) LECLERC D.
PA   (WILS/) WILSON A.
PA   (ROSE/) ROSENBLATT D.
Query Match
Best Local Similarity 22.8%;   Score 71.5;   DB 9;   Pred. No. 1.2e+02;   Length 698;

RESULT 1143
ID   ADQ39858 standard; protein; 725 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1521.
PN   US20040058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 22.8%;   Score 71.5;   DB 8;   Pred. No. 1.2e+02;   Length 725;

RESULT 1144
ID   ADU06586 standard; protein; 725 AA.
DE   Novel bronchial cancer-associated human protein SeqID812.
PN   DE10316701-A1.
PD   04-NOV-2004.
PA   (HINZ/) HINZMANN B.
PA   (HERM/) HERMANN K.
Query Match
Best Local Similarity 22.8%;   Score 71.5;   DB 8;   Pred. No. 1.2e+02;   Length 725;

RESULT 1145
ID   AAY51606 standard; protein; 890 AA.
DE   Human wml protein.
PN   DE19845277-C1.
PD   09-MAR-2000.
PA   (UYMU/) UNIV MUENCHEN MAXIMILIANS LUDWIG.
Query Match
Best Local Similarity 22.8%;   Score 71.5;   DB 3;   Pred. No. 1.5e+02;   Length 890;

RESULT 1146
ID   ABB78282 standard; protein; 890 AA.
DE   Amino acid sequence of human wolframin polypeptide.
PN   WO200263307-A2.
PD   15-AUG-2002.
PA   (PHAR) PHARMACIA & UPJOHN CO.
PA   (PHA) PHARMACIA & UPJOHN CO.
Query Match
Best Local Similarity 23.8%;   Score 71.5;   DB 5;   Pred. No. 1.5e+02;   Length 890;

RESULT 1147
ID   ADD46013 standard; protein; 890 AA.
DE   Human Protein O76024, SEQ ID NO 11685.
PN   WO20030164755-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
Query Match
Best Local Similarity 23.8%;   Score 71.5;   DB 7;   Pred. No. 1.5e+02;   Length 890;

RESULT 1148
ID   ADF69127 standard; protein; 890 AA.
DE   Human MP53 protein sequence SEQ ID NO:97.
PN   WO200383047-A2.
PD   09-OCT-2003.
PA   (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 23.8%;   Score 71.5;   DB 7;   Pred. No. 1.5e+02;   Length 890;

RESULT 1149
ID   ADY70426 standard; protein; 890 AA.
DE   Human beta-amyloid precursor protein, wolframin.
PN   WO200502385B-A1.
PD   17-MAR-2005.
PA   (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 23.8%;   Score 71.5;   DB 9;   Pred. No. 1.5e+02;   Length 890;

RESULT 1150
ID   ADY70680 standard; protein; 890 AA.
DE   Human nicastrin/Psen2-complex member, wolframin protein.
PN   WO200502383J-A2.
PD   17-MAR-2005.
PA   (CELL/) CELLZOME AG.
Query Match
Best Local Similarity 23.8%;   Score 71.5;   DB 9;   Pred. No. 1.5e+02;   Length 890;

RESULT 1151
ID   AEE39892 standard; protein; 890 AA.
DE   Amino acid sequence SEQ ID NO:24.
PN   WO200511297B-A2.
PD   01-DEC-2005.
PA   (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 23.8%;   Score 71.5;   DB 9;   Pred. No. 1.5e+02;   Length 890;

RESULT 1152
ID   ADL22689 standard; protein; 2245 AA.
DE   Human disease detection and treatment (MDDT) protein - SEQ ID 138.
PN   WO2003062799-A2.
PD   31-JUL-2003.
PA   (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 22.4%;   Score 71.5;   DB 7;   Pred. No. 6.1e+02;   Length 2245;

RESULT 1153
ID   AAB42192 standard; protein; 2405 AA.
DE   Human ORFX ORF1956 polypeptide sequence SEQ ID NO:3912.
PN   WO200058473-A2.
PD   05-OCT-2000.
PA   (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 22.4%;   Score 71.5;   DB 3;   Pred. No. 5.5e+02;   Length 2405;

RESULT 1154
ID   ABB11404 standard; peptide; 2560 AA.
DE   Human FLAMINGO 1 homologue, SEQ ID NO:1774.
PN   WO200157188-A2.
PD   09-AUG-2001.
PA   (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 22.4%;   Score 71.5;   DB 6;   Pred. No. 6.6e+02;   Length 2560;

RESULT 1155
ID   ABU11556 standard; protein; 2894 AA.
DE   Human MDDT polypeptide SEQ ID 503.
PN   WO200279449-A2.
PD   10-OCT-2002.
PA   (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 22.4%;   Score 71.5;   DB 6;   Pred. No. 7.9e+02;   Length 2894;

RESULT 1156
ID   AAU07054 standard; protein; 2923 AA.
DE   Human Flamingo protein encoded by cDNA splice variant.
PN   WO200161003-A1.
PD   23-AUG-2001.

RESULT 1147

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PA  (SMIK )  SMITHKLINE BEECHAM PLC.
    Query Match    6.0%;   Score 71.5;  DB 4;  Length 2923;
    Best Local Similarity    22.4%;   Pred. No. 8e+02;
RESULT 1157
ID  AAM50866 standard; protein; 2923 AA.
DE  Cadherin EGF LAG seven-pass G-type receptor 2, basal cell marker.
PN  WO020208765-A2.
PD  31-JAN-2002.
PA  (STRD )  UNIV STANFORD.
PA  (GENO-)  APPLIED GENOMICS INC.
    Query Match    6.0%;   Score 71.5;  DB 5;  Length 2923;
    Best Local Similarity    22.4%;   Pred. No. 8e+02;
RESULT 1158
ID  ABP82018 standard; protein; 2923 AA.
DE  Human GPCR CELSR2 protein SEQ ID NO:524.
PN  WO020261087-A2.
PD  08-AUG-2002.
PA  (LIFE-)  LIFESPAN BIOSCIENCES INC.
    Query Match    6.0%;   Score 71.5;  DB 6;  Length 2923;
    Best Local Similarity    22.4%;   Pred. No. 8e+02;
RESULT 1159
ID  ADC15499 standard; protein; 2923 AA.
DE  Human cadherin EGF LAG seven-pass G-type receptor 2.
PN  US20030865934-A1.
PD  08-MAY-2003.
PA  (BOTS/)  BOTSTEIN D.
PA  (BROW/)  BROWN P O.
PA  (PERO/)  PEROU C M.
PA  (RING/)  RING B.
PA  (ROSS/)  ROSS D.
PA  (SEIT/)  SEITZ R.
PA  (VRIJ/)  VAN DE RIJN J M.
    Query Match    6.0%;   Score 71.5;  DB 7;  Length 2923;
    Best Local Similarity    22.4%;   Pred. No. 8e+02;
RESULT 1160
ID  ADC86479 standard; protein; 2923 AA.
DE  Human GPCR protein SEQ ID NO:932.
PN  EP1270724-A2.
PD  02-JAN-2003.
PA  (NAAD-)  NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA  (ADSC-)  CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
    Query Match    6.0%;   Score 71.5;  DB 7;  Length 2923;
    Best Local Similarity    22.4%;   Pred. No. 8e+02;
RESULT 1161
ID  ADE54407 standard; protein; 2923 AA.
DE  Human Protein XP_042739, SEQ ID NO 210.
PN  WO2003016475-A2.
PD  27-FEB-2003.
PA  (GEHO )  GEN HOSPITAL CORP.
    Query Match    6.0%;   Score 71.5;  DB 7;  Length 2923;
    Best Local Similarity    22.4%;   Pred. No. 8e+02;
RESULT 1162
ID  ADE54411 standard; protein; 2923 AA.
DE  Human Protein XP_042739, SEQ ID NO 214.
PN  WO2003016475-A2.
PD  27-FEB-2003.
PA  (GEHO )  GEN HOSPITAL CORP.
    Query Match    6.0%;   Score 71.5;  DB 7;  Length 2923;
    Best Local Similarity    22.4%;   Pred. No. 8e+02;
RESULT 1163
ID  AD029245 standard; protein; 2923 AA.
DE  Human GPCR CELSR2, SEQ ID NO:346.
PN  WO2004040000-A2.
PD  13-MAY-2004.
PA  (PRIM-)  PRIMAL INC.
    Query Match    6.0%;   Score 71.5;  DB 8;  Length 2923;
    Best Local Similarity    22.4%;   Pred. No. 8e+02;
RESULT 1164
ID  ADY70314 standard; protein; 2923 AA.
DE  Human beta-APP, cadherin EGF LAG seven-pass G-type receptor 2.
PN  WO2005023858-A1.
PD  17-MAR-2005.
PA  (CELL-)  CELLZOME AG.
    Query Match    6.0%;   Score 71.5;  DB 9;  Length 2923;
    Best Local Similarity    22.4%;   Pred. No. 8e+02;
RESULT 1165
ID  ADY70652 standard; protein; 2923 AA.
DE  Human BACE1/PTK7-complex member, CELSR2 protein.
PN  WO2005023833-A2.
PD  17-MAR-2005.
PA  (CELL-)  CELLZOME AG.
    Query Match    6.0%;   Score 71.5;  DB 9;  Length 2923;
    Best Local Similarity    22.4%;   Pred. No. 8e+02;
RESULT 1166
ID  ADY70648 standard; protein; 2923 AA.
DE  Human BACE1-complex, cadherin seven-pass G-type receptor 2 protein.
PN  WO2005023833-A2.
PD  17-MAR-2005.
PA  (CELL-)  CELLZOME AG.
    Query Match    6.0%;   Score 71.5;  DB 5;  Length 2936;
    Best Local Similarity    22.4%;   Pred. No. 8e+02;
RESULT 1167
ID  AAU74826 standard; protein; 2936 AA.
DE  Human REPTR 9 protein.
PN  WO200198354-A2.
PD  27-DEC-2001.
PA  (INCY-)  INCYTE GENOMICS INC.
    Query Match    6.0%;   Score 71.5;  DB 4;  Length 2956;
    Best Local Similarity    22.4%;   Pred. No. 8.1e+02;
RESULT 1168
ID  AAU07053 standard; protein; 2956 AA.
DE  Human Flamingo polypeptide.
PN  WO200161003-A1.
PD  23-AUG-2001.
PA  (SMIK )  SMITHKLINE BEECHAM PLC.
    Query Match    6.0%;   Score 71.5;  DB 9;  Length 3010;
    Best Local Similarity    23.7%;   Pred. No. 8.3e+02;
RESULT 1169
ID  ADX40788 standard; protein; 3010 AA.
DE  HCV polymerase protein #11.
PN  WO2005012502-A2.
PD  10-FEB-2005.
PA  (EPIM-)  EPIMMUNE INC.
    Query Match    6.0%;   Score 71.5;  DB 9;  Length 3011;
    Best Local Similarity    23.7%;   Pred. No. 8.3e+02;
RESULT 1170
ID  AAR34468 standard; protein; 3011 AA.
DE  Encoded by full-length Hepatitis C virus clone JK1-B.
PN  JP05068562-A.
PD  23-MAR-1993.
PA  (SANW )  SANWA KAGAKU KENKYUSHO CO.
    Query Match    6.0%;   Score 71.5;  DB 2;  Length 3011;
    Best Local Similarity    23.7%;   Pred. No. 8.3e+02;
RESULT 1171
ID  AAR31621 standard; protein; 3011 AA.
DE  Hepatitis C virus (HCV) polyprotein.
PN  WO930365-A2.
PD  07-JAN-1993.
PA  (CHIR )  CHIRON CORP.
    Query Match    6.0%;   Score 71.5;  DB 2;  Length 3011;
    Best Local Similarity    22.8%;   Pred. No. 8.3e+02;
RESULT 1172
ID  ABB67866 standard; protein; 5303 AA.
DE  Drosophila melanogaster polypeptide SEQ ID NO 30390.
PN  WO200171042-A2.
PD  27-SEP-2001.
PA  (PEKE )  PE CORP NY.
    Query Match    6.0%;   Score 71.5;  DB 4;  Length 5303;
    Best Local Similarity    29.5%;   Pred. No. 1.8e+03;
RESULT 1173
ID  AEF50785 standard; protein; 195 AA.
DE  MmsC A8 clone, hypothetical transmembrane protein #1.
PN  WO2006005943-A1.
PD  19-JAN-2006.
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PA   (MORE-) MOREDUN RES INST.
     Query Match   5.9%; Score 71; DB 10; Length 195;
     Best Local Similarity 25.0%; Pred. No. 21;

RESULT 1174
ID   ABB06793 standard; protein; 198 AA.
DE   Human transmembrane 4 protein 22 SEQ ID NO:2.
PN   CN127990-A.
PD   26-DEC-2001.
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
     Query Match   5.9%; Score 71; DB 5; Length 198;
     Best Local Similarity 24.5%; Pred. No. 22;

RESULT 1175
ID   AEC21170 standard; protein; 217 AA.
DE   L. acidophilus metal-dependent membrane protease #6.
PN   WO2005081959-A2.
PD   09-SEP-2005.
PA   (UYNC-) UNIV NORTH CAROLINA STATE.
     Query Match   5.9%; Score 71; DB 9; Length 217;
     Best Local Similarity 22.4%; Pred. No. 25;

RESULT 1176
ID   ADU08919 standard; protein; 223 AA.
DE   Coronavirus membrane protein seqid 42.
PN   WO2004096842-A2.
PD   11-NOV-2004.
PA   (BCCA-) BC CANCER AGENCY.
     Query Match   5.9%; Score 71; DB 8; Length 223;
     Best Local Similarity 22.4%; Pred. No. 26;

RESULT 1177
ID   ABR58398 standard; protein; 240 AA.
DE   Human NOV17a.
PN   WO2003029423-A2.
PD   10-APR-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match   5.9%; Score 71; DB 6; Length 240;
     Best Local Similarity 18.6%; Pred. No. 28;

RESULT 1178
ID   ABP26255 standard; protein; 295 AA.
DE   Streptococcus polypeptide SEQ ID NO 1686.
PN   WO200234771-A2.
PD   02-MAY-2002.
PA   (CHIR-) CHIRON SPA.
PA   (GENO-) INST GENOMIC RES.
     Query Match   5.9%; Score 71; DB 5; Length 295;
     Best Local Similarity 24.9%; Pred. No. 38;

RESULT 1179
ID   ADX65958 standard; protein; 309 AA.
DE   Plant full length insert polypeptide seqid 36801.
PN   US20040034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match   5.9%; Score 71; DB 8; Length 309;
     Best Local Similarity 18.7%; Pred. No. 40;

RESULT 1180
ID   AAG72952 standard; protein; 310 AA.
DE   Human olfactory receptor data exploratorium sequence, SEQ ID NO: 2634.
PN   WO200127158-A2.
PD   19-APR-2001.
PA   (DIGI-) DIGISCENTS.
PA   (YEDA) YEDA RES & DEV CO LTD.
     Query Match   5.9%; Score 71; DB 4; Length 310;
     Best Local Similarity 22.9%; Pred. No. 41;

RESULT 1181
ID   AAR48717 standard; protein; 312 AA.
DE   G-protein coupled human interleukin-8 receptor protein.
PN   WO9405695-A1.
PD   17-MAR-1994.
PA   (UYNY) UNIV NEW YORK STATE.
     Query Match   5.9%; Score 71; DB 2; Length 312;
     Best Local Similarity 19.7%; Pred. No. 41;

RESULT 1182
ID   AAW02689 standard; peptide; 312 AA.
DE   G-protein coupled human interleukin-8 receptor.
PN   US5508384-A.
PD   16-APR-1996.
PA   (UYNY) UNIV NEW YORK STATE.
     Query Match   5.9%; Score 71; DB 2; Length 312;
     Best Local Similarity 19.7%; Pred. No. 41;

RESULT 1183
ID   AAG72169 standard; protein; 312 AA.
DE   Human olfactory receptor polypeptide, SEQ ID NO: 1850.
PN   WO200127158-A2.
PD   19-APR-2001.
PA   (DIGI-) DIGISCENTS.
PA   (YEDA) YEDA RES & DEV CO LTD.
     Query Match   5.9%; Score 71; DB 4; Length 312;
     Best Local Similarity 22.9%; Pred. No. 41;

RESULT 1184
ID   AAG72377 standard; protein; 312 AA.
DE   Human OR-like polypeptide query sequence, SEQ ID NO: 2058.
PN   WO200127158-A2.
PD   19-APR-2001.
PA   (DIGI-) DIGISCENTS.
PA   (YEDA) YEDA RES & DEV CO LTD.
     Query Match   5.9%; Score 71; DB 4; Length 312;
     Best Local Similarity 22.9%; Pred. No. 41;

RESULT 1185
ID   ADY08080 standard; protein; 364 AA.
DE   Plant full length insert polypeptide seqid 63895.
PN   US20040034888-A1.
PD   19-FEB-2004.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match   5.9%; Score 71; DB 8; Length 364;
     Best Local Similarity 18.7%; Pred. No. 51;

RESULT 1186
ID   AEF93343 standard; protein; 382 AA.
DE   Canis sphingosine-1-phosphate isoform 1 (cS1P1) receptor.
PN   WO2006014802-A2.
PD   09-FEB-2006.
PA   (MERI) MERCK & CO INC.
     Query Match   5.9%; Score 71; DB 10; Length 382;
     Best Local Similarity 20.5%; Pred. No. 54;

RESULT 1187
ID   ABB54394 standard; protein; 391 AA.
DE   Lactococcus lactis protein ykiI.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG) INRA INST NAT RECH AGRONOMIQUE.
     Query Match   5.9%; Score 71; DB 5; Length 391;
     Best Local Similarity 20.3%; Pred. No. 56;

RESULT 1188
ID   ABB48413 standard; protein; 423 AA.
DE   Listeria monocytogenes protein #1068.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP) INST PASTEUR.
     Query Match   5.9%; Score 71; DB 5; Length 423;
     Best Local Similarity 28.4%; Pred. No. 62;

RESULT 1189
ID   ADL05302 standard; protein; 423 AA.
DE   M. catarrhalis protein #1068.
PN   US6673910-B1.
PD   06-JAN-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   5.9%; Score 71; DB 8; Length 423;
     Best Local Similarity 38.0%; Pred. No. 62;

RESULT 1190

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ID   ADJ95142 standard; protein; 444 AA.
PN   WO2003040325-A2.
DE   Novel NOVX protein sequence #185.
PD   15-MAY-2003.
PA   (CURA-) CURAGEN CORP.
Query Match        5.9%;  Score 71;  DB 7;  Length 444;
Best Local Similarity   21.0%;  Pred. No. 67;

RESULT 1191
ID   ADJ95144 standard; protein; 444 AA.
PN   WO2003040325-A2.
DE   Novel NOVX protein sequence #186.
PD   15-MAY-2003.
PA   (CURA-) CURAGEN CORP.
Query Match        5.9%;  Score 71;  DB 7;  Length 444;
Best Local Similarity   21.0%;  Pred. No. 67;

RESULT 1192
ID   ADU73808 standard; protein; 448 AA.
PN   WO2004099388-A2.
DE   Drosophila melanogaster Cbl-b.
PD   18-NOV-2004.
PA   (PROT-) PROTEOLOGICS INC.
Query Match        5.9%;  Score 71;  DB 8;  Length 448;
Best Local Similarity   23.5%;  Pred. No. 68;

RESULT 1193
ID   ADU69155 standard; protein; 448 AA.
PN   WO2004098492-A2.
DE   Drosophila melanogaster Cbl-B protein.
PD   18-NOV-2004.
PA   (PROT-) PROTEOLOGICS INC.
Query Match        5.9%;  Score 71;  DB 8;  Length 448;
Best Local Similarity   23.5%;  Pred. No. 68;

RESULT 1194
ID   ADW87442 standard; protein; 448 AA.
PN   WO2005007141-A2.
DE   Fruit fly CBL-B protein.
PD   27-JAN-2005.
PA   (PROT-) PROTEOLOGICS INC.
Query Match        5.9%;  Score 71;  DB 9;  Length 448;
Best Local Similarity   23.5%;  Pred. No. 68;

RESULT 1195
ID   ADP29417 standard; protein; 455 AA.
PN   WO2004035732-A2.
DE   Human secreted protein SEQ ID #1415.
PD   29-APR-2004.
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match        5.9%;  Score 71;  DB 8;  Length 455;
Best Local Similarity   24.3%;  Pred. No. 69;

RESULT 1196
ID   ABU19912 standard; protein; 457 AA.
PN   WO2002277183-A2.
DE   Protein encoded by Prokaryotic essential gene #5439.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match        5.9%;  Score 71;  DB 6;  Length 457;
Best Local Similarity   22.0%;  Pred. No. 69;

RESULT 1197
ID   ADI24575 standard; protein; 470 AA.
PN   US2003224442-A1.
DE   Human endogenous 5HT2A serotonin receptor.
PD   04-DEC-2003.
PA   (CHAL/) CHALMERS D T.
PA   (BEHA/) BEHAN D P.
PA   (LIAW/) LIAW C W.
PA   (RUSS/) RUSSO J F.
PA   (THOM/) THOMSEN W J.
Query Match        5.9%;  Score 71;  DB 8;  Length 470;
Best Local Similarity   23.7%;  Pred. No. 72;

RESULT 1198
ID   AAR37659 standard; protein; 471 AA.
DE   Sequence encoded by cDNA.
PN   WO9311257-A2.
PD   10-JUN-1993.
PA   (BOEH) BOEHRINGER INGELHEIM INT GMBH.
Query Match        5.9%;  Score 71;  DB 2;  Length 471;
Best Local Similarity   23.7%;  Pred. No. 72;

RESULT 1199
ID   AAW23781 standard; protein; 471 AA.
DE   Human serotonin 5-HT2 receptor protein.
PN   US5561024-A.
PD   26-AUG-1997.
PA   (SYNA-) SYNAPTIC PHARM CORP.
Query Match        5.9%;  Score 71;  DB 2;  Length 471;
Best Local Similarity   23.7%;  Pred. No. 72;

RESULT 1200
ID   AAW77107 standard; protein; 471 AA.
DE   Human 5-HT2A serotonin receptor.
PN   WO9838217-A1.
PD   03-SEP-1998.
PA   (TEIT/) TEITLER M.
PA   (HERR/) HERRICK-DAVIS K.
PA   (EGAN/) EGAN C C.
Query Match        5.9%;  Score 71;  DB 2;  Length 471;
Best Local Similarity   23.7%;  Pred. No. 72;

RESULT 1201
ID   AAY90640 standard; protein; 471 AA.
DE   Human G protein-coupled receptor 5HT-2A (serotonin receptor).
PN   WO2002022129-A1.
PD   20-APR-2000.
PA   (AREN-) ARENA PHARM INC.
Query Match        5.9%;  Score 71;  DB 3;  Length 471;
Best Local Similarity   23.7%;  Pred. No. 72;

RESULT 1202
ID   AAY90675 standard; protein; 471 AA.
DE   Human mutant G protein-coupled receptor 5HT-2A.
PN   WO2002022129-A1.
PD   20-APR-2000.
PA   (AREN-) ARENA PHARM INC.
Query Match        5.9%;  Score 71;  DB 3;  Length 471;
Best Local Similarity   23.7%;  Pred. No. 72;

RESULT 1203
ID   ABB07978 standard; protein; 471 AA.
DE   Human 5-HT2 receptor sequence.
PN   US6383762-B1.
PD   07-MAY-2002.
PA   (SYNA-) SYNAPTIC PHARM CORP.
Query Match        5.9%;  Score 71;  DB 5;  Length 471;
Best Local Similarity   23.7%;  Pred. No. 72;

RESULT 1204
ID   ABP81765 standard; protein; 471 AA.
DE   Human 5-HT2A receptor protein SEQ ID NO:12.
PN   WO200261087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match        5.9%;  Score 71;  DB 6;  Length 471;
Best Local Similarity   23.7%;  Pred. No. 72;

RESULT 1205
ID   ADC22641 standard; protein; 471 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #32.
PN   US6555339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
Query Match        5.9%;  Score 71;  DB 7;  Length 471;
Best Local Similarity   23.7%;  Pred. No. 72;

RESULT 1206
ID   ADC22747 standard; protein; 471 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #72.
PN   US6555339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
Query Match        5.9%;  Score 71;  DB 7;  Length 471;
Best Local Similarity   23.7%;  Pred. No. 72;

RESULT 1207
ID   ADE65844 standard; protein; 471 AA.
DE   Human serotonin 2A receptor.
PN   US2003170723-A1.
PD   11-SEP-2003.
PA   (AREN-) ARENA PHARM INC.
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PA   (SATO/) SATO T.
Query Match

RESULT 1208
Best Local Similarity   23.7%;   Score 71;   DB 7;   Pred. No. 72;   Length 471;
ID   ADH14220 standard; protein; 471 AA.
DE   Mutated human serotonin 5HT_2A.
PN   US2003105292-A1.
PD   05-JUN-2003.
PA   (LIAW/) LIAW C W.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.

RESULT 1209
Query Match
Best Local Similarity   23.7%;   Score 71;   DB 7;   Pred. No. 72;   Length 471;
ID   ADH14114 standard; protein; 471 AA.
DE   Human serotonin 5HT_2A.
PN   US2003105292-A1.
PD   05-JUN-2003.
PA   (LIAW/) LIAW C W.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.

RESULT 1210
Query Match
Best Local Similarity   23.7%;   Score 71;   DB 7;   Pred. No. 72;   Length 471;
ID   ADL90125 standard; protein; 471 AA.
DE   Human serotonin receptor 5HT2a.
PN   US2003167476-A1.
PD   04-SEP-2003.
PA   (CONK/) CONKLIN B R.

RESULT 1211
Query Match
Best Local Similarity   23.7%;   Score 71;   DB 7;   Pred. No. 72;   Length 471;
ID   ADQ29506 standard; protein; 471 AA.
DE   Human GPCR HTR2A, SEQ ID NO:608.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.

RESULT 1212
Query Match
Best Local Similarity   23.7%;   Score 71;   DB 8;   Pred. No. 72;   Length 471;
ID   ADQ39800 standard; protein; 471 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1463.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.

RESULT 1213
Query Match
Best Local Similarity   23.7%;   Score 71;   DB 8;   Pred. No. 72;   Length 471;
ID   ADQ39799 standard; protein; 471 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1462.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.

RESULT 1214
Query Match
Best Local Similarity   23.7%;   Score 71;   DB 8;   Pred. No. 72;   Length 471;
ID   ADQ39798 standard; protein; 471 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1461.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.

RESULT 1215
Query Match
Best Local Similarity   23.7%;   Score 71;   DB 8;   Pred. No. 72;   Length 471;
ID   ADU48367 standard; protein; 471 AA.
DE   Human serotonin 2A receptor protein.
PN   US2004229287-A1.
PD   18-NOV-2004.
PA   (UYCO) UNIV COLUMBIA NEW YORK.

RESULT 1216
Query Match
Best Local Similarity   23.7%;   Score 71;   DB 8;   Pred. No. 72;   Length 471;
ID   ADX02782 standard; protein; 471 AA.
DE   Human 5-HT 2a receptor protein SeqID22.
PN   WO2005012254-A1.
PD   10-FEB-2005.
PA   (AREN-) ARENA PHARM INC.

RESULT 1217
Query Match
Best Local Similarity   23.7%;   Score 71;   DB 9;   Pred. No. 72;   Length 471;
ID   AEF70361 standard; protein; 471 AA.
DE   Human 5-hydroxytryptamine 2A receptor protein sequence.
PN   WO2006010515-A2.
PD   02-FEB-2006.
PA   (FARB) BAYER HEALTHCARE AG.

RESULT 1218
Query Match
Best Local Similarity   23.7%;   Score 71;   DB 10;   Pred. No. 74;   Length 478;
ID   AAY01626 standard; protein; 478 AA.
DE   Amino acid sequence of the human 5-HT2 receptor.
PN   US5885785-A.
PD   23-MAR-1999.
PA   (SYNA-) SYNAPTIC PHARM CORP.

RESULT 1219
Query Match
Best Local Similarity   23.7%;   Score 71;   DB 2;   Pred. No. 74;   Length 480;
ID   ABG70577 standard; protein; 480 AA.
DE   Human serotonin (5-HT2) receptor.
PN   US2002009548-A1.
PD   25-JUL-2002.
PA   (SYNA-) SYNAPTIC PHARM CORP.

RESULT 1220
Query Match
Best Local Similarity   23.7%;   Score 71;   DB 5;   Pred. No. 77;   Length 493;
ID   ABM70440 standard; protein; 493 AA.
DE   Photorhabdus luminescens protein sequence #3537.
PN   WO2002094867-A2.
PD   28-NOV-2002.
PA   (INSP) INST PASTEUR.
PA   (CNRS) CNRS CENT NAT RECH SCI.

RESULT 1221
Query Match
Best Local Similarity   23.5%;   Score 71;   DB 6;   Pred. No. 89;   Length 545;
ID   ADE56383 standard; protein; 545 AA.
DE   Rat Protein O70536, SEQ ID NO 2235.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.

RESULT 1222
Query Match
Best Local Similarity   22.0%;   Score 71;   DB 7;   Pred. No. 89;   Length 545;
ID   ADD48660 standard; protein; 545 AA.
DE   Rat Protein BAA25372, SEQ ID NO 14366.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO) GEN HOSPITAL CORP.

RESULT 1223
Query Match
Best Local Similarity   22.0%;   Score 71;   DB 7;   Pred. No. 89;   Length 546;
ID   ADS43584 standard; protein; 546 AA.
DE   Bacterial polypeptide #22014.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.

RESULT 1224
Query Match
Best Local Similarity   26.2%;   Score 71;   DB 8;   Pred. No. 89;   Length 546;
ID   ABJ26399 standard; protein; 559 AA.
DE   Aspergillus fumigatus essential gene protein #1057.
PN   WO2002086090-A2.

PD   31-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   5.9%;   Score 71;   DB 6;   Length 559;
Best Local Similarity 23.1%;   Pred. No. 92;
RESULT 1225
ID   ABP35686 standard; protein; 563 AA.
DE   Fungal 2BC protein sequence #112.
PN   WO200224865-A2.
PD   28-MAR-2002.
PA   (MICR-) MICROBIA INC.
Query Match   5.9%;   Score 71;   DB 5;   Length 563;
Best Local Similarity 19.1%;   Pred. No. 93;
RESULT 1226
ID   AAB20578 standard; protein; 564 AA.
DE   Mouse OCTN3 protein SEQ ID NO:1.
PN   WO200046368-A1.
PD   10-AUG-2000.
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
PA   (NIGA/) NIGAM S K.
PA   (ERAL/) ERALY S A.
Query Match   5.9%;   Score 71;   DB 3;   Length 564;
Best Local Similarity 21.4%;   Pred. No. 93;
RESULT 1227
ID   AED51410 standard; protein; 564 AA.
DE   Novel organic cation transporter (OCTN) protein, MOCTN3, SEQ ID NO: 83.
PN   US2005241012-A1.
PD   27-OCT-2005.
PA   (NIGA/) NIGAM S K.
PA   (ERAL/) ERALY S A.
Query Match   5.9%;   Score 71;   DB 9;   Length 564;
Best Local Similarity 21.4%;   Pred. No. 93;
RESULT 1228
ID   AEB36506 standard; protein; 603 AA.
DE   L. pneumophila protein SEQ ID NO 838.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP) INST PASTEUR.
PA   (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA   (CNRS) CNRS CENT NAT RECH SCI.
Query Match   5.9%;   Score 71;   DB 9;   Length 603;
Best Local Similarity 18.3%;   Pred. No. 1e+02;
RESULT 1229
ID   ADQ96374 standard; protein; 631 AA.
DE   T cell activation associated protein #276.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match   5.9%;   Score 71;   DB 8;   Length 631;
Best Local Similarity 21.3%;   Pred. No. 1.1e+02;
RESULT 1230
ID   ADQ96376 standard; protein; 631 AA.
DE   T cell activation associated protein #277.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match   5.9%;   Score 71;   DB 8;   Length 631;
Best Local Similarity 21.3%;   Pred. No. 1.1e+02;
RESULT 1231
ID   ABB91532 standard; protein; 676 AA.
DE   Herbicidally active polypeptide SEQ ID NO 743.
PN   WO2002102010-A2.
PD   07-FEB-2002.
PA   (FARB) BAYER AG.
Query Match   5.9%;   Score 71;   DB 5;   Length 676;
Best Local Similarity 21.3%;   Pred. No. 1.2e+02;
RESULT 1232
ID   AAE21800 standard; protein; 727 AA.
DE   Human HIPHUM 0000029 protein.
PN   GB2365432-A.
PD   20-FEB-2002.
PA   (GLAX) GLAXO GROUP LTD.
Query Match   5.9%;   Score 71;   DB 5;   Length 727;
Best Local Similarity 24.3%;   Pred. No. 1.3e+02;
RESULT 1233

ID   ABU54636 standard; protein; 727 AA.
DE   Human NOVX polypeptide #95.
PN   WO200281498-A2.
PD   17-OCT-2002.
PA   (CURA-) CURAGEN CORP.
Query Match   5.9%;   Score 71;   DB 6;   Length 727;
Best Local Similarity 24.3%;   Pred. No. 1.3e+02;
RESULT 1234
ID   ADH76500 standard; protein; 727 AA.
DE   727 amino acid human neurotransmitter transporter protein.
PN   US2003219774-A1.
PD   27-NOV-2003.
PA   (SHAR/) SHARMA R.
PA   (RAMA/) RAMANATHAN C S.
PA   (WEST/) WESTPHAL R.
PA   (FEDE/) FEDER J N.
PA   (LEEL/) LEE L M.
Query Match   5.9%;   Score 71;   DB 8;   Length 727;
Best Local Similarity 24.3%;   Pred. No. 1.3e+02;
RESULT 1235
ID   AEF11189 standard; protein; 742 AA.
DE   HCV protein BP208/FLF SEQ ID NO:44.
PN   WO2006001517-A1.
PD   05-JAN-2006.
PA   (ADIT-) ADVANCED LIFE SCI INST INC.
Query Match   5.9%;   Score 71;   DB 10;   Length 742;
Best Local Similarity 24.8%;   Pred. No. 1.4e+02;
RESULT 1236
ID   ABR62929 standard; protein; 744 AA.
DE   Human neurotransmitter transporter.
PN   WO2003059947-A1.
PD   24-JUL-2003.
PA   (FARB) BAYER AG.
Query Match   5.9%;   Score 71;   DB 7;   Length 744;
Best Local Similarity 24.3%;   Pred. No. 1.4e+02;
RESULT 1237
ID   ABB60052 standard; protein; 792 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 6948.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
Query Match   5.9%;   Score 71;   DB 4;   Length 792;
Best Local Similarity 17.7%;   Pred. No. 1.5e+02;
RESULT 1238
ID   ABM90462 standard; protein; 929 AA.
DE   Rice abiotic stress responsive polypeptide SEQ ID NO:9184.
PN   WO2003008540-A2.
PD   30-JAN-2003.
PA   (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match   5.9%;   Score 71;   DB 7;   Length 929;
Best Local Similarity 20.6%;   Pred. No. 1.9e+02;
RESULT 1239
ID   AAR30616 standard; protein; 3010 AA.
DE   Blood transmissible NANBHV protein.
PN   JP06105690-A.
PD   19-APR-1994.
PA   (KAEN/) KAENNO K.
Query Match   5.9%;   Score 71;   DB 2;   Length 3010;
Best Local Similarity 26.9%;   Pred. No. 9.5e+02;
RESULT 1240
ID   AAR53417 standard; protein; 3010 AA.
DE   Polypeptide coded by Korean HCV full cDNA sequence LBC1.
PN   EP521318-A2.
PD   07-JAN-1993.
PA   (LUCK-) LUCKY LTD.
Query Match   5.9%;   Score 71;   DB 2;   Length 3010;
Best Local Similarity 26.9%;   Pred. No. 9.5e+02;
RESULT 1241
ID   ADX40817 standard; protein; 3010 AA.
DE   HCV polymerase protein #40.
PN   WO2005012502-A2.
PD   10-FEB-2005.
PA   (EPIM-) EPIMMUNE INC.

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     Query Match            26.9%;   Score 71;   Pred. No. 9.5e+02;   DB 9;   Length 3010;
     Best Local Similarity  26.9%;

RESULT 1242
ID   ADX40783 standard; protein; 3010 AA.
DE   HCV polymerase protein #6.
PN   WO2005012502-A2.
PD   10-FEB-2005.
PA   (EPIM-) EPIMMUNE INC.
     Query Match            26.9%;   Score 71;   Pred. No. 9.5e+02;   DB 9;   Length 3010;
     Best Local Similarity  26.9%;

RESULT 1243
ID   ADX40812 standard; protein; 3010 AA.
DE   HCV polymerase protein #35.
PN   WO2005012502-A2.
PD   10-FEB-2005.
PA   (EPIM-) EPIMMUNE INC.
     Query Match            26.9%;   Score 71;   Pred. No. 9.5e+02;   DB 9;   Length 3010;
     Best Local Similarity  26.9%;

RESULT 1244
ID   ABR85573 standard; protein; 202 AA.
DE   BcrC amino acid sequence SEQ ID NO:40.
PN   WO2003057708-A2.
PD   17-JUL-2003.
PA   (UYNE-) UNIV NEWCASTLE VENTURES LTD.
     Query Match            26.5%;   Score 71;   Pred. No. 9.5e+02;   DB 6;   Length 202;
     Best Local Similarity  26.9%;

RESULT 1245
ID   AAU01287 standard; protein; 218 AA.
DE   Brassica napus fatty acid desaturase, Fad3C, partial sequence.
PN   WO2001025453-A2.
PD   12-APR-2001.
PA   (MIAC ) CANADA MIN AGRIC & AGRI-FOOD CANADA.
     Query Match            29.3%;   Score 70.5;   Pred. No. 29;   DB 4;   Length 218;
     Best Local Similarity  29.3%;

RESULT 1246
ID   AAU97208 standard; protein; 228 AA.
DE   Portion of a wheat sugar transport protein encoded by wrein.pk0006.b4.
PN   US6383776-B1.
PD   07-MAY-2002.
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
     Query Match             5.9%;   Score 70.5;   Pred. No. 30;   DB 5;   Length 228;
     Best Local Similarity  21.6%;

RESULT 1247
ID   AAU08333 standard; protein; 228 AA.
DE   Wheat sugar transport protein #3.
PN   US2002178468-A1.
PD   28-NOV-2002.
PA   (ALLE/) ALLEN S M.
PA   (HITZ/) HITZ W D.
PA   (KINN/) KINNEY A J.
PA   (TING/) TINGEY S V.
     Query Match             5.9%;   Score 70.5;   Pred. No. 30;   DB 6;   Length 228;
     Best Local Similarity  21.6%;

RESULT 1248
ID   ADG47920 standard; protein; 228 AA.
DE   Wheat Arabidopsis-like sugar transport protein #3.
PN   US2002199217-A1.
PD   26-DEC-2002.
PA   (ALLE/) ALLEN S M.
PA   (HITZ/) HITZ W D.
PA   (KINN/) KINNEY A J.
PA   (TING/) TINGEY S V.
PA   (HELE/) HELENTJARIS T G.
     Query Match             5.9%;   Score 70.5;   Pred. No. 30;   DB 8;   Length 228;
     Best Local Similarity  21.6%;

RESULT 1249
ID   AEE68531 standard; protein; 228 AA.
DE   Triticum aestivum sugar transport protein amino acid sequence SEQ ID 16.
PN   US2005282278-A1.
PD   22-DEC-2005.
PA   (ALLE/) ALLEN S M.
PA   (HITZ/) HITZ W D.
PA   (KINN/) KINNEY A J.
PA   (TING/) TINGEY S V.
     Query Match             5.9%;   Score 70.5;   Pred. No. 30;   DB 10;   Length 228;
     Best Local Similarity  21.6%;

RESULT 1250
ID   ABU17430 standard; protein; 275 AA.
DE   Protein encoded by Prokaryotic essential gene #2957.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match             5.9%;   Score 70.5;   Pred. No. 39;   DB 6;   Length 275;
     Best Local Similarity  22.8%;

RESULT 1251
ID   ADY06253 standard; protein; 283 AA.
DE   Plant full length insert polypeptide seqid 62068.
PN   US2004034888-A1.
PD   19-FEB-2004.
PA   (ELIT-) ELITRA PHARM INC.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
     Query Match             5.9%;   Score 70.5;   Pred. No. 41;   DB 8;   Length 283;
     Best Local Similarity  27.4%;

RESULT 1252
ID   ABB55033 standard; protein; 285 AA.
DE   Lactococcus lactis protein malG.
PN   FR2807446-A1.
PD   12-OCT-2001.
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
     Query Match             5.9%;   Score 70.5;   Pred. No. 41;   DB 5;   Length 285;
     Best Local Similarity  26.1%;

RESULT 1253
ID   ABB05467 standard; protein; 291 AA.
DE   Coriolus versicolor aldo/ketoreductase protein SEQ ID NO:2.
PN   JP2001321171-A.
PD   20-NOV-2001.
PA   (KUBI ) KUBOTA CORP.
PA   (WARI/) WARIISHI H.
     Query Match             5.9%;   Score 70.5;   Pred. No. 43;   DB 5;   Length 291;
     Best Local Similarity  29.4%;

RESULT 1254
ID   ADA35787 standard; protein; 297 AA.
DE   Acinetobacter baumannii protein #2948.
PN   US6562956-B1.
PD   13-MAY-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match             5.9%;   Score 70.5;   Pred. No. 44;   DB 6;   Length 297;
     Best Local Similarity  24.1%;

RESULT 1255
ID   ABM70358 standard; protein; 321 AA.
DE   Photorhabdus luminescens protein sequence #3455.
PN   WO2002094867-A2.
PD   28-NOV-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
     Query Match             5.9%;   Score 70.5;   Pred. No. 49;   DB 6;   Length 321;
     Best Local Similarity  19.2%;

RESULT 1256
ID   ADH22355 standard; protein; 330 AA.
DE   Human receptor & membrane associated protein (REMAP) SeqID5.
PN   WO2003104395-A2.
PD   18-DEC-2003.
PA   (INCY-) INCYTE CORP.
     Query Match             5.9%;   Score 70.5;   Pred. No. 51;   DB 8;   Length 330;
     Best Local Similarity  24.2%;

RESULT 1257
ID   ADK68232 standard; protein; 343 AA.
DE   Novel NOVX protein #79.
PN   WO2003085124-A2.
PD   16-OCT-2003.
PA   (CURA-) CURAGEN CORP.
     Query Match             5.9%;   Score 70.5;   Pred. No. 53;   DB 7;   Length 343;
     Best Local Similarity  30.0%;

RESULT 1258
ID   ADH72226 standard; protein; 343 AA.
DE   Human protein of the invention NOV55a SEQ ID NO:1122.
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PN   WO2003102155-A2.
PD   11-DEC-2003.
PA   (CURA-) CURAGEN CORP.
Query Match   30.0%; Score 70.5; DB 8; Length 343;
Best Local Similarity   30.0%; Pred. No. 53;

RESULT 1259
ID   ADR49221 standard; protein; 343 AA.
DE   Human NOV10a protein.
PN   US2004162236-A1.
PD   19-AUG-2004.
PA   (ALSO/) ALSOBROOK J.
PA   (BENT/) BENTO P.
PA   (BOLD/) BOLDOG F.
PA   (BURG/) BURGESS C.
PA   (CASM/) CASMAN S.
PA   (BOKO/) BOKOR J C.
PA   (EDIN/) EDINGER S R.
PA   (ELLE/) ELLERMAN K.
PA   (FERN/) FERNANDES E.
PA   (GERL/) GERLACH V.
PA   (GROS/) GROSSE W.
PA   (GUNT/) GUNTHER E.
PA   (GUSE/) GUSEV V.
PA   (HEYE/) HEYES M.
PA   (LEPL/) LEPLEY D.
PA   (LILL/) LI L.
PA   (MACD/) MACDOUGALL J R.
PA   (MALY/) MALYANKAR U M.
PA   (MILL/) MILLET I.
PA   (PEYM/) PEYMAN J A.
PA   (PATT/) PATTURAJAN M.
PA   (RAST/) RASTELLI L.
PA   (RIEG/) RIEGER D.
PA   (SHEN/) SHENOY S.
PA   (SHIM/) SHIMKETS R.
PA   (SMIT/) SMITHSON G.
PA   (STON/) STONE D.
PA   (VERN/) VERNET C.
PA   (VOSS/) VOSS E.
Query Match   5.9%; Score 70.5; DB 8; Length 343;
Best Local Similarity   30.0%; Pred. No. 53;

RESULT 1260
ID   ADY15182 standard; protein; 350 AA.
DE   PRO polypeptide SEQ ID NO 988.
PN   WO2005016962-A2.
PD   24-FEB-2005.
PA   (GETH) GENENTECH INC.
Query Match   5.9%; Score 70.5; DB 9; Length 350;
Best Local Similarity   18.5%; Pred. No. 55;

RESULT 1261
ID   ADY15180 standard; protein; 350 AA.
DE   PRO polypeptide SEQ ID NO 986.
PN   WO2005016962-A2.
PD   24-FEB-2005.
PA   (GETH) GENENTECH INC.
Query Match   5.9%; Score 70.5; DB 9; Length 350;
Best Local Similarity   18.5%; Pred. No. 55;

RESULT 1262
ID   ADR40543 standard; protein; 363 AA.
DE   Ovine melatonin receptor O46608 protein.
PN   US2004161823-A1.
PD   19-AUG-2004.
PA   (FEDE/) FEDER J N.
PA   (MINT/) MINTIER G.
PA   (RAMA/) RAMANATHAN C S.
PA   (HAWK/) HAWKEN D R.
Query Match   5.9%; Score 70.5; DB 8; Length 363;
Best Local Similarity   23.1%; Pred. No. 58;

RESULT 1263
ID   AAR69518 standard; protein; 365 AA.
DE   Prostaglandin-EP3-9 receptor.
PN   WO9505052-A1.
PD   05-JAN-1995.
PA   (MERI) MERCK FROSST CANADA INC.
Query Match   5.9%; Score 70.5; DB 2; Length 365;
Best Local Similarity   24.2%; Pred. No. 58;

RESULT 1264
ID   AAE38521 standard; protein; 365 AA.
DE   Human PTGER3 protein isoform, EP3b.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
Query Match   5.9%; Score 70.5; DB 7; Length 365;
Best Local Similarity   24.2%; Pred. No. 58;

RESULT 1265
ID   ADI35077 standard; protein; 365 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #9.
PN   US2003224493-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
Query Match   5.9%; Score 70.5; DB 8; Length 365;
Best Local Similarity   24.2%; Pred. No. 58;

RESULT 1266
ID   ADI15889 standard; protein; 365 AA.
DE   Human prostaglandin EP3 receptor #3.
PN   US6670134-B1.
PD   30-DEC-2003.
PA   (ALLE) ALLERGAN INC.
PA   (UYAR-) UNIV ARIZONA.
Query Match   5.9%; Score 70.5; DB 8; Length 365;
Best Local Similarity   24.2%; Pred. No. 58;

RESULT 1267
ID   ADR67864 standard; protein; 365 AA.
DE   Prostaglandin E2 EP3 III.
PN   WO2004074830-A2.
PD   02-SEP-2004.
PA   (FARB) BAYER HEALTHCARE AG.
Query Match   5.9%; Score 70.5; DB 8; Length 365;
Best Local Similarity   24.2%; Pred. No. 58;

RESULT 1268
ID   ADS21429 standard; protein; 366 AA.
DE   Bacterial polypeptide #10462.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
Query Match   5.9%; Score 70.5; DB 8; Length 366;
Best Local Similarity   21.2%; Pred. No. 59;

RESULT 1269
ID   ADF04358 standard; protein; 367 AA.
DE   Bacterial polypeptide #471.
PN   US6605709-B1.
PD   12-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match   5.9%; Score 70.5; DB 7; Length 367;
Best Local Similarity   21.2%; Pred. No. 59;

RESULT 1270
ID   AAE38520 standard; protein; 374 AA.
DE   Human PTGER3 protein isoform, EP3d.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
Query Match   5.9%; Score 70.5; DB 7; Length 374;
Best Local Similarity   33.3%; Pred. No. 60;

RESULT 1271
ID   ADI35075 standard; protein; 374 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #8.
PN   US2003224493-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
Query Match   5.9%; Score 70.5; DB 8; Length 374;
Best Local Similarity   24.2%; Pred. No. 60;

RESULT 1272

ID   AAR48711 standard; protein; 379 AA.
DE   G-protein coupled rat serotonin 2 receptor protein.
PN   WO9405695-A1.
PD   17-MAR-1994.
PA   (UYNY) UNIV NEW YORK STATE.
     Query Match   5.9%; Score 22.9%; DB 2; Length 379;
     Best Local Similarity 22.9%; Pred. No. 61;
RESULT 1273

ID   AAW02683 standard; peptide; 379 AA.
DE   G-protein coupled rat serotonin 2 receptor.
PN   US5508384-A.
PD   16-APR-1996.
PA   (UYNY) UNIV NEW YORK STATE.
     Query Match   5.9%; Score 22.9%; DB 2; Length 379;
     Best Local Similarity 22.9%; Pred. No. 61;
RESULT 1274

ID   AAR69517 standard; protein; 388 AA.
DE   Prostaglandin-EP3-21 receptor.
PN   WO9500552-A1.
PD   05-JAN-1995.
PA   (MERI) MERCK FROSST CANADA INC.
     Query Match   5.9%; Score 70.5; DB 2; Length 388;
     Best Local Similarity 24.2%; Pred. No. 63;
RESULT 1275

ID   AAE38513 standard; protein; 388 AA.
DE   Human PTGER3 protein isoform, EP3c.
PN   WO200306447l-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match   5.9%; Score 70.5; DB 7; Length 388;
     Best Local Similarity 24.2%; Pred. No. 63;
RESULT 1276

ID   ADI35061 standard; protein; 388 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #1.
PN   US200322433-A1.
PD   04-DEC-2003.
PA   (ALLR) ALLERGAN INC.
     Query Match   5.9%; Score 70.5; DB 8; Length 388;
     Best Local Similarity 24.2%; Pred. No. 63;
RESULT 1277

ID   ADI15887 standard; protein; 388 AA.
DE   Human prostaglandin EP3 receptor #2.
PN   US6670134-B1.
PD   30-DEC-2003.
PA   (UYAR-) UNIV ARIZONA.
     Query Match   5.9%; Score 70.5; DB 8; Length 388;
     Best Local Similarity 24.2%; Pred. No. 63;
RESULT 1278

ID   ADS13753 standard; protein; 388 AA.
DE   Human prostaglandin E2 EP3 II polypeptide.
PN   WO2004075813-A2.
PD   10-SEP-2004.
PA   (FARB) BAYER HEALTHCARE AG.
     Query Match   5.9%; Score 70.5; DB 8; Length 388;
     Best Local Similarity 24.2%; Pred. No. 63;
RESULT 1279

ID   AAR69516 standard; protein; 390 AA.
DE   Prostaglandin-EP3-alpha receptor.
PN   WO9500552-A1.
PD   05-JAN-1995.
PA   (MERI) MERCK FROSST CANADA INC.
     Query Match   5.9%; Score 70.5; DB 2; Length 390;
     Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1280

ID   AAE38516 standard; protein; 390 AA.
DE   Human PTGER3 protein isoform, EP3a1.
PN   WO200306447l-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match   5.9%; Score 70.5; DB 7; Length 390;
     Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1281

ID   AAE38517 standard; protein; 390 AA.
DE   Human PTGER3 protein isoform, EP3a2.
PN   WO200306447l-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match   5.9%; Score 70.5; DB 7; Length 390;
     Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1282

ID   ADI35067 standard; protein; 390 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #4.
PN   US200322433-A1.
PD   04-DEC-2003.
PA   (ALLR) ALLERGAN INC.
     Query Match   5.9%; Score 70.5; DB 8; Length 390;
     Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1283

ID   ADI35069 standard; protein; 390 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #5.
PN   US200322433-A1.
PD   04-DEC-2003.
PA   (ALLR) ALLERGAN INC.
     Query Match   5.9%; Score 70.5; DB 8; Length 390;
     Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1284

ID   ADI15898 standard; protein; 390 AA.
DE   Human prostaglandin EP3 receptor #4.
PN   US6670134-B1.
PD   30-DEC-2003.
PA   (UYAR-) UNIV ARIZONA.
     Query Match   5.9%; Score 70.5; DB 8; Length 390;
     Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1285

ID   ADI15885 standard; protein; 390 AA.
DE   Human prostaglandin EP3 receptor #1.
PN   US6670134-B1.
PD   30-DEC-2003.
PA   (UYAR-) UNIV ARIZONA.
     Query Match   5.9%; Score 70.5; DB 8; Length 390;
     Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1286

ID   ADR70434 standard; protein; 390 AA.
DE   Human prostaglandin E2 EP3 protein.
PN   WO2004074842-A2.
PD   02-SEP-2004.
PA   (FARB) BAYER HEALTHCARE AG.
     Query Match   5.9%; Score 70.5; DB 8; Length 390;
     Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1287

ID   ADS76168 standard; protein; 390 AA.
DE   Human prostaglandin E2 EP3 I.
PN   WO2004075814-A2.
PD   10-SEP-2004.
PA   (FARB) BAYER HEALTHCARE AG.
     Query Match   5.9%; Score 70.5; DB 8; Length 390;
     Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1288

ID   AEF06389 standard; protein; 390 AA.
DE   Human PGE receptor type 3a2 SEQ ID NO 7.
PN   WO2005085851-A2.
PD   15-SEP-2005.
PA   (ADRA/) ADRA C N.
     Query Match   5.9%; Score 70.5; DB 10; Length 390;
     Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1289

ID   AAW57411 standard; protein; 393 AA.
DE   Human prostaglandin EP3-VI receptor.
PN   JP1013185-A.
PD   06-MAY-1998.
PA   (ONOY) ONO PHARM CO LTD.
     Query Match   5.9%; Score 70.5; DB 2; Length 393;
     Best Local Similarity 24.2%; Pred. No. 65;

RESULT 1290
ID   AAE38519 standard; protein; 393 AA.
DE   Human PTGER3 protein isoform, EP3e.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match   5.9%;   Score 70.5;   DB 7;   Length 393;
     Best Local Similarity   24.2%;   Pred. No. 65;

RESULT 1291
ID   AAE38523 standard; protein; 393 AA.
DE   Human PTGER3 protein isoform, EP3-VI.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match   5.9%;   Score 70.5;   DB 7;   Length 393;
     Best Local Similarity   24.2%;   Pred. No. 65;

RESULT 1292
ID   ADI35081 standard; protein; 393 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #11.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match   5.9%;   Score 70.5;   DB 8;   Length 393;
     Best Local Similarity   24.2%;   Pred. No. 65;

RESULT 1293
ID   ADI35073 standard; protein; 393 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #7.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match   5.9%;   Score 70.5;   DB 8;   Length 393;
     Best Local Similarity   24.2%;   Pred. No. 65;

RESULT 1294
ID   AAW57410 standard; protein; 402 AA.
DE   Human EP3-V receptor.
PN   JP10111318S-A.
PD   06-MAY-1998.
PA   (ONOY) ONO PHARM CO LTD.
     Query Match   5.9%;   Score 70.5;   DB 2;   Length 402;
     Best Local Similarity   24.2%;   Pred. No. 67;

RESULT 1295
ID   ABP81904 standard; protein; 402 AA.
DE   Human prostaglandin E2 receptor EP3 protein SEQ ID NO:294.
PN   WO2002061087-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
     Query Match   5.9%;   Score 70.5;   DB 6;   Length 402;
     Best Local Similarity   24.2%;   Pred. No. 67;

RESULT 1296
ID   AAB38522 standard; protein; 402 AA.
DE   Human PTGER3 protein isoform, EP3-V.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match   5.9%;   Score 70.5;   DB 7;   Length 402;
     Best Local Similarity   24.2%;   Pred. No. 67;

RESULT 1297
ID   ADI35079 standard; protein; 402 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #10.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match   5.9%;   Score 70.5;   DB 8;   Length 402;
     Best Local Similarity   24.2%;   Pred. No. 67;

RESULT 1298
ID   AD55167 standard; protein; 402 AA.
DE   Protein #69 with increased gene expression in renal cell carcinoma.
PN   WO2004032842-A2.
PD   22-APR-2004.
PA   (VAND-) VAN ANDEL INST.
     Query Match   5.9%;   Score 70.5;   DB 8;   Length 402;
     Best Local Similarity   24.2%;   Pred. No. 67;

RESULT 1299

ID   ADO29620 standard; protein; 402 AA.
DE   Human GPCR PTGER3, SEQ ID NO:722.
PN   WO200404000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
     Query Match   5.9%;   Score 70.5;   DB 8;   Length 402;
     Best Local Similarity   24.2%;   Pred. No. 67;

RESULT 1300
ID   ADZ09834 standard; protein; 402 AA.
DE   Human breast cancer marker DKFZp586M0723 protein.
PN   EP1522594-A2.
PD   13-APR-2005.
PA   (FARB) BAYER HEALTHCARE AG.
     Query Match   5.9%;   Score 70.5;   DB 9;   Length 402;
     Best Local Similarity   24.2%;   Pred. No. 67;

RESULT 1301
ID   AAB38514 standard; protein; 407 AA.
DE   Human PTGER3 protein isoform, EP3g.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match   5.9%;   Score 70.5;   DB 7;   Length 407;
     Best Local Similarity   24.2%;   Pred. No. 68;

RESULT 1302
ID   ADI35063 standard; protein; 407 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #2.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match   5.9%;   Score 70.5;   DB 8;   Length 407;
     Best Local Similarity   24.2%;   Pred. No. 68;

RESULT 1303
ID   AAB38518 standard; protein; 425 AA.
DE   Human PTGER3 protein isoform, EP3f.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match   5.9%;   Score 70.5;   DB 7;   Length 425;
     Best Local Similarity   24.2%;   Pred. No. 72;

RESULT 1304
ID   ADI35071 standard; protein; 425 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #6.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match   5.9%;   Score 70.5;   DB 8;   Length 425;
     Best Local Similarity   24.2%;   Pred. No. 72;

RESULT 1305
ID   AEF77677 standard; protein; 425 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER2) variant 1.
PN   WO2006011171-A2.
PD   16-FEB-2006.
PA   (META-) METABOLEX INC.
     Query Match   5.9%;   Score 70.5;   DB 10;   Length 425;
     Best Local Similarity   24.2%;   Pred. No. 74;

RESULT 1306
ID   AAB38515 standard; protein; 433 AA.
DE   Human PTGER3 protein isoform, EP3h.
PN   WO2003064471-A2.
PD   07-AUG-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match   5.9%;   Score 70.5;   DB 7;   Length 433;
     Best Local Similarity   24.2%;   Pred. No. 74;

RESULT 1307
ID   ADI35065 standard; protein; 433 AA.
DE   Human prostaglandin E receptor subtype EP3 (PTGER3) protein #3.
PN   US2003224393-A1.
PD   04-DEC-2003.
PA   (DECO-) DECODE GENETICS EHF.
     Query Match   5.9%;   Score 70.5;   DB 8;   Length 433;
     Best Local Similarity   24.2%;   Pred. No. 74;

RESULT 1308
ID   AAW98431 standard; protein; 480 AA.

DE   H. pylori GHPO 446 protein.
PN   WO9843478-A1.
PD   08-OCT-1998.
PN   US2005282278-A1.
PA   (INNR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (ALLE/) ALLEN S M.
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
Query Match   23.1%;   Score 70.5;   DB 2;   Length 480;
Best Local Similarity   5.9%;   Pred. No. 85;
RESULT 1309
ID   ADY09805 standard; protein; 494 AA.
DE   Plant full length insert polypeptide seqid 65620.
PN   US20040034888-A1.
PD   19-FEB-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
PA   (BUSH/) BUSH D.
PA   (DOUC/) DOUCETTE-STAMM L.
Query Match   21.4%;   Score 70.5;   DB 8;   Length 494;
Best Local Similarity   5.9%;   Pred. No. 89;
RESULT 1310
ID   ABP40525 standard; protein; 499 AA.
DE   Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5370.
PN   US6380370-B1.
PD   30-APR-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   20.5%;   Score 70.5;   DB 5;   Length 499;
Best Local Similarity   5.9%;   Pred. No. 90;
RESULT 1311
ID   ABS06092 standard; protein; 499 AA.
DE   Staphylococcus epidermidis polypeptide seqid 5387.
PN   US20040147734-A1.
PD   29-JUL-2004.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   20.5%;   Score 70.5;   DB 8;   Length 499;
Best Local Similarity   5.9%;   Pred. No. 90;
RESULT 1312
ID   ABU30473 standard; protein; 521 AA.
DE   Protein encoded by Prokaryotic essential gene #16000.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   23.7%;   Score 70.5;   DB 6;   Length 521;
Best Local Similarity   5.9%;   Pred. No. 95;
RESULT 1313
ID   AAU97213 standard; protein; 539 AA.
DE   Wheat sugar transport protein #4.
PN   US2002178468-A1.
PD   28-NOV-2002.
PA   (DUPO) DU PONT DE NEMOURS & CO E I.
PA   (ALLE/) ALLEN S M.
PA   (HITZ/) HITZ W D.
PA   (KINN/) KINNEY A J.
PA   (TING/) TINGEY S V.
Query Match   26.0%;   Score 70.5;   DB 5;   Length 539;
Best Local Similarity   5.9%;   Pred. No. 1e+02;
RESULT 1314
ID   ABU08338 standard; protein; 539 AA.
DE   Wheat sugar transport protein #1.
PN   US2002199217-A1.
PD   26-DEC-2002.
PA   (DUPO) DU PONT DE NEMOURS & CO E I.
PA   (ALLE/) ALLEN S M.
PA   (HITZ/) HITZ W D.
PA   (KINN/) KINNEY A J.
PA   (TING/) TINGEY S V.
PA   (HELE/) HELENTJARIS T G.
Query Match   26.0%;   Score 70.5;   DB 6;   Length 539;
Best Local Similarity   5.9%;   Pred. No. 1e+02;
RESULT 1315
ID   ADG47930 standard; protein; 539 AA.
DE   Wheat Beta-vulgaris-like sugar transport protein #1.
Query Match   26.0%;   Score 70.5;   DB 5;   Length 539;
Best Local Similarity   5.9%;   Pred. No. 1e+02;
RESULT 1316
ID   AEE68541 standard; protein; 539 AA.
DE   Triticum aestivum sugar transport protein amino acid sequence SEQ ID 26.
PN   US2005282278-A1.
PD   22-DEC-2005.
PA   (ALLE/) ALLEN S M.
PA   (HITZ/) HITZ W D.
PA   (KINN/) KINNEY A J.
PA   (TING/) TINGEY S V.
Query Match   26.0%;   Score 70.5;   DB 10;   Length 539;
Best Local Similarity   5.9%;   Pred. No. 1e+02;
RESULT 1317
ID   ABU27418 standard; protein; 548 AA.
DE   Protein encoded by Prokaryotic essential gene #12945.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   24.0%;   Score 70.5;   DB 6;   Length 548;
Best Local Similarity   5.9%;   Pred. No. 1e+02;
RESULT 1318
ID   ADN2789 standard; protein; 556 AA.
DE   Bacterial polypeptide #5442.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
Query Match   21.1%;   Score 70.5;   DB 8;   Length 556;
Best Local Similarity   5.9%;   Pred. No. 1e+02;
RESULT 1319
ID   ADD46023 standard; protein; 599 AA.
DE   Rat Protein P23978, SEQ ID NO 11695.
PN   WO2003016475-A2.
PD   27-FEB-2003.
PA   (GEHO/) GEN HOSPITAL CORP.
PA   (FARB) BAYER AG.
Query Match   20.1%;   Score 70.5;   DB 7;   Length 599;
Best Local Similarity   5.9%;   Pred. No. 1.2e+02;
RESULT 1320
ID   ABW02687 standard; protein; 599 AA.
DE   Rattus norvegicus neuronal GABA transporter (GAT-1).
PN   US2003143729-A1.
PD   31-JUL-2003.
PA   (SYNA-) SYNAPTIC PHARM CORP.
Query Match   20.1%;   Score 70.5;   DB 7;   Length 599;
Best Local Similarity   5.9%;   Pred. No. 1.2e+02;
RESULT 1321
ID   AAM78767 standard; protein; 600 AA.
DE   Human protein SEQ ID NO 1429.
PN   WO200157190-A2.
PD   09-AUG-2001.
PA   (HYSE-) HYSEQ INC.
Query Match   19.5%;   Score 70.5;   DB 4;   Length 600;
Best Local Similarity   5.9%;   Pred. No. 1.2e+02;
RESULT 1322
ID   ADJ64315 standard; protein; 662 AA.
DE   Cartilage differentiation inhibiting protein, SEQ ID 10.
PN   WO2004013326-A1.
PD   12-FEB-2004.
PA   (ASAH) ASAHI KASEI KK.
Query Match   22.7%;   Score 70.5;   DB 8;   Length 662;
Best Local Similarity   5.9%;   Pred. No. 1.3e-02;
RESULT 1323
ID   ABB92892 standard; protein; 700 AA.
DE   Herbicidally active polypeptide SEQ ID NO 2103.
PN   WO200210210-A2.
PD   07-FEB-2002.
PA   (FARB) BAYER AG.
Query Match   25.8%;   Score 70.5;   DB 5;   Length 700;
Best Local Similarity   5.9%;   Pred. No. 1.4e+02;
RESULT 1324
ID   AAB56721 standard; protein; 717 AA.

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DE   Human prostate cancer antigen protein sequence SEQ ID NO:1299.
PN   WO200055174-A1.
PD   21-SEP-2000.
PA   (ROSE/) ROSEN C A.
PA   (HUMA-) HUMAN GENOME SCI INC.
RESULT 1325
  Best Local Similarity 22.4%;    Score 70.5; DB 3; Length 717;
  Query Match            5.9%;    Pred. No. 1.5e+02;
ID   ADG47941 standard; protein; 740 AA.
DE   Arabidopsis thaliana-like sugar transport protein #2.
PN   US20021992171-A1.
PD   26-DEC-2002.
PA   (HELE/) HELENTJARIS T G.
RESULT 1326
  Best Local Similarity 22.8%;    Score 70.5; DB 8; Length 740;
  Query Match            5.9%;    Pred. No. 1.6e+02;
ID   AAG39555 standard; protein; 766 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 48959.
PN   EP1033405-A2.
PD   06-SEP-2000.
RESULT 1327
  Best Local Similarity 21.3%;    Score 70.5; DB 3; Length 766;
  Query Match            5.9%;    Pred. No. 1.6e+02;
ID   AAG39554 standard; protein; 815 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 48958.
PN   EP1033405-A2.
PD   06-SEP-2000.
RESULT 1328
  Best Local Similarity 21.3%;    Score 70.5; DB 3; Length 815;
  Query Match            5.9%;    Pred. No. 1.8e+02;
ID   AAG39553 standard; protein; 927 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 48957.
PN   EP1033405-A2.
PD   06-SEP-2000.
RESULT 1329
  Best Local Similarity 21.3%;    Score 70.5; DB 3; Length 927;
  Query Match            5.9%;    Pred. No. 2.1e+02;
ID   ABP73754 standard; protein; 1026 AA.
DE   Candida albicans essential protein SEQ ID NO 7591.
PN   WO200253728-A2.
PD   11-JUL-2002.
RESULT 1330
  Best Local Similarity 22.3%;    Score 70.5; DB 5; Length 1026;
  Query Match            5.9%;    Pred. No. 2.4e+02;
ID   AAW17057 standard; protein; 1027 AA.
DE   Candida albicans chitin synthase (CHS1).
PN   WO9716540-A1.
PD   09-MAY-1997.
PA   (ELIT-) ELITRA PHARM INC.
RESULT 1331
  Best Local Similarity 22.3%;    Score 70.5; DB 8; Length 1027;
  Query Match            5.9%;    Pred. No. 2.4e+02;
ID   ADH22510 standard; protein; 1147 AA.
DE   Human transporter & ion channel (TRICH) protein SeqID8.
PN   WO2003093444-A2.
PD   13-NOV-2003.
PA   (INCY-) INCYTE CORP.
RESULT 1332
  Best Local Similarity 19.5%;    Score 70.5; DB 8; Length 1147;
  Query Match            5.9%;    Pred. No. 2.9e+02;
ID   ADK18350 standard; protein; 1163 AA.
DE   Human NOVX protein #2.
PN   WO2003057854-A2.
PD   17-JUL-2003.
PA   (CURA-) CURAGEN CORP.
RESULT 1333
  Best Local Similarity 19.5%;    Score 70.5; DB 7; Length 1163;
  Query Match            5.9%;    Pred. No. 2.9e+02;
ID   ADM29274 standard; protein; 1163 AA.
DE   Human novel protein NOV2b.
PN   WO2003064628-A2.
PD   07-AUG-2003.

PA   (CURA-) CURAGEN CORP.
RESULT 1334
  Best Local Similarity 19.5%;    Score 70.5; DB 7; Length 1163;
  Query Match            5.9%;    Pred. No. 2.9e+02;
ID   AAW53863 standard; peptide; 1780 AA.
DE   Human gravin polypeptide.
PN   US5741890-A.
PD   21-APR-1998.
PA   (UYOR-) UNIV OREGON HEALTH SCI.
RESULT 1335
  Best Local Similarity 34.8%;    Score 70.5; DB 2; Length 1780;
  Query Match            5.9%;    Pred. No. 5.2e+02;
ID   AAB15380 standard; protein; 1780 AA.
DE   Human gravin protein sequence.
PN   US6090929-A.
PD   18-JUL-2000.
PA   (UYOR-) UNIV OREGON HEALTH SCI.
RESULT 1336
  Best Local Similarity 34.8%;    Score 70.5; DB 3; Length 1780;
  Query Match            5.9%;    Pred. No. 5.2e+02;
ID   AAO17365 standard; protein; 1781 AA.
DE   Human gravin.
PN   EP1191107-A2.
PD   27-MAR-2002.
PA   (SCHD ) SCHERING AG.
RESULT 1337
  Best Local Similarity 34.8%;    Score 70.5; DB 5; Length 1781;
  Query Match            5.9%;    Pred. No. 5.2e+02;
ID   ABU03477 standard; protein; 1781 AA.
DE   Angiogenesis-associated human protein sequence #22.
PN   WO200279492-A2.
PD   10-OCT-2002.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
RESULT 1338
  Best Local Similarity 34.8%;    Score 70.5; DB 6; Length 1781;
  Query Match            5.9%;    Pred. No. 5.2e+02;
ID   ABB97448 standard; protein; 1783 AA.
DE   Novel human protein SEQ ID NO: 716.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
RESULT 1339
  Best Local Similarity 34.8%;    Score 70.5; DB 5; Length 1783;
  Query Match            5.9%;    Pred. No. 5.3e+02;
ID   ABG21018 standard; protein; 1795 AA.
DE   Novel human diagnostic protein #21009.
PN   WO200226660-A2.
PD   21-MAR-2002.
PA   (HYSE-) HYSEQ INC.
RESULT 1340
  Best Local Similarity 34.8%;    Score 70.5; DB 4; Length 1795;
  Query Match            5.9%;    Pred. No. 5.3e+02;
ID   AAG34242 standard; protein; 185 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 41630.
PN   EP1033405-A2.
PD   06-SEP-2000.
RESULT 1341
  Best Local Similarity 26.2%;    Score 70; DB 3; Length 185;
  Query Match            5.9%;    Pred. No. 26;
ID   AAG34241 standard; protein; 189 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 41631.
PN   EP1033405-A2.
PD   06-SEP-2000.
RESULT 1342
  Best Local Similarity 26.2%;    Score 70; DB 3; Length 189;
  Query Match            5.9%;    Pred. No. 27;
ID   AAW44944 standard; protein; 225 AA.
DE   Avian infectious bronchitis virus glycoprotein M.
PN   FR2751225-A1.
PD   23-JAN-1998.
PA   (INMR ) RHONE MERIEUX SA.
  Best Local Similarity 21.6%;    Score 70; DB 2; Length 225;
  Query Match            5.9%;    Pred. No. 34;
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RESULT 1343
ID   AD809893 standard; protein; 226 AA.
DE   Alloiococcus otitis antigenic protein SEQ ID NO:3730.
PN   WO200304830-A2.
PD   12-JUN-2003.
PA   (AMP ) WYETH HOLDINGS CORP.
Query Match             5.9%;  Score 70;  DB 6;  Length 226;
Best Local Similarity  24.1%;  Pred. No. 34;

RESULT 1344
ID   AAG34240 standard; protein; 235 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 41629.
PN   EP103405-A2.
PD   06-SEP-2000.
Query Match             5.9%;  Score 70;  DB 3;  Length 235;
Best Local Similarity  26.2%;  Pred. No. 36;

RESULT 1345
ID   ABB69790 standard; protein; 256 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 36162.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE ) PE CORP NY.
Query Match             5.9%;  Score 70;  DB 4;  Length 256;
Best Local Similarity  20.2%;  Pred. No. 41;

RESULT 1346
ID   ADS96502 standard; protein; 256 AA.
DE   Drosophila melanogaster protein, SEQ ID 123.
PN   WO200403999-A2.
PD   13-MAY-2004.
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
Query Match             5.9%;  Score 70;  DB 8;  Length 256;
Best Local Similarity  20.2%;  Pred. No. 41;

RESULT 1347
ID   AD705703 standard; protein; 256 AA.
DE   Haemophilus influenzae (NThi) protein - SEQ ID 739.
PN   WO200407889-A2.
PD   16-SEP-2004.
PA   (CHIL-) CHILDRENS HOSPITAL INC.
Query Match             5.9%;  Score 70;  DB 8;  Length 256;
Best Local Similarity  18.3%;  Pred. No. 41;

RESULT 1348
ID   AAG53761 standard; protein; 274 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 68478.
PN   EP103405-A2.
PD   06-SEP-2000.
Query Match             5.9%;  Score 70;  DB 3;  Length 274;
Best Local Similarity  26.0%;  Pred. No. 45;

RESULT 1349
ID   AAG53762 standard; protein; 287 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 68477.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match             5.9%;  Score 70;  DB 3;  Length 287;
Best Local Similarity  26.0%;  Pred. No. 48;

RESULT 1350
ID   ABU35677 standard; protein; 292 AA.
DE   Protein encoded by Prokaryotic essential gene #21204.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match             5.9%;  Score 70;  DB 6;  Length 292;
Best Local Similarity  22.5%;  Pred. No. 49;

RESULT 1351
ID   ADK48488 standard; protein; 307 AA.
DE   Streptococcus pneumoniae protein, Seq ID No 5003.
PN   US6699703-B1.
PD   02-MAR-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match             5.9%;  Score 70;  DB 8;  Length 307;
Best Local Similarity  26.2%;  Pred. No. 52;

RESULT 1352
ID   AAR72985 standard; protein; 333 AA.
DE   Epsilon opioid receptor.
PN   WO9512670-A1.
PD   11-MAY-1995.
PA   (ALCO-) ALCOHOLISM & DRUG ADDICTION RES FOUND.
Query Match             5.9%;  Score 70;  DB 2;  Length 333;
Best Local Similarity  23.6%;  Pred. No. 59;

RESULT 1353
ID   AAY90613 standard; protein; 333 AA.
DE   Human G protein-coupled receptor GPR8.
PN   WO200222129-A1.
PD   20-APR-2000.
PA   (AREN-) ARENA PHARM INC.
Query Match             5.9%;  Score 70;  DB 3;  Length 333;
Best Local Similarity  23.6%;  Pred. No. 59;

RESULT 1354
ID   AAY90647 standard; protein; 333 AA.
DE   Human mutant G protein-coupled receptor GPR8 (T259K).
PN   WO200222129-A1.
PD   20-APR-2000.
PA   (AREN-) ARENA PHARM INC.
Query Match             5.9%;  Score 70;  DB 3;  Length 333;
Best Local Similarity  23.6%;  Pred. No. 59;

RESULT 1355
ID   AAU01297 standard; protein; 333 AA.
DE   Human G-protein coupled receptor 8, GPR 8, mutant N127A.
PN   WO200127632-A2.
PD   19-APR-2001.
PA   (CAMB-) CAMBRIDGE DRUG DISCOVERY LTD.
Query Match             5.9%;  Score 70;  DB 4;  Length 333;
Best Local Similarity  23.6%;  Pred. No. 59;

RESULT 1356
ID   AAU01295 standard; protein; 333 AA.
DE   Human G-protein coupled receptor 8, GPR 8.
PN   WO200127632-A2.
PD   19-APR-2001.
PA   (CAMB-) CAMBRIDGE DRUG DISCOVERY LTD.
Query Match             5.9%;  Score 70;  DB 4;  Length 333;
Best Local Similarity  23.6%;  Pred. No. 59;

RESULT 1357
ID   AAU01298 standard; protein; 333 AA.
DE   Human G-protein coupled receptor 8, GPR 8, mutant T259E.
PN   WO200127632-A2.
PD   19-APR-2001.
PA   (CAMB-) CAMBRIDGE DRUG DISCOVERY LTD.
Query Match             5.9%;  Score 70;  DB 4;  Length 333;
Best Local Similarity  23.6%;  Pred. No. 59;

RESULT 1358
ID   ABB84683 standard; protein; 333 AA.
DE   Human GPR8-ligand related protein #1.
PN   WO200198494-A1.
PD   27-DEC-2001.
PA   (TAKE ) TAKEDA CHEM IND LTD.
Query Match             5.9%;  Score 70;  DB 5;  Length 333;
Best Local Similarity  23.6%;  Pred. No. 59;

RESULT 1359
ID   ABB84723 standard; protein; 333 AA.
DE   Human GPR8-ligand related protein #3.
PN   WO200198494-A1.
PD   27-DEC-2001.
PA   (TAKE ) TAKEDA CHEM IND LTD.
Query Match             5.9%;  Score 70;  DB 5;  Length 333;
Best Local Similarity  23.6%;  Pred. No. 59;

RESULT 1360
ID   ABG65918 standard; protein; 333 AA.
DE   G protein-coupled receptor related peptide #6.
PN   WO200244368-A1.
PD   06-JUN-2002.
PA   (TAKE ) TAKEDA CHEM IND LTD.
Query Match             5.9%;  Score 70;  DB 5;  Length 333;
Best Local Similarity  23.6%;  Pred. No. 59;

RESULT 1361
ID   ABU61448 standard; protein; 333 AA.
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DE   Screening method related protein #1.
PN   WO20029161-A1.
PD   21-NOV-2002.
PA   (TAKE) TAKEDA CHEM IND LTD.
      Query Match   5.9%;   Score 70;   DB 6;   Length 333;
      Best Local Similarity   23.6%;   Pred. No. 59;

RESULT 1362
ID   ABJ37874 standard; protein; 333 AA.
DE   GPR7 ligand related human protein SEQ ID No 84.
PN   WO20102847-A1.
PD   27-DEC-2002.
PA   (TAKE) TAKEDA CHEM IND LTD.
      Query Match   5.9%;   Score 70;   DB 6;   Length 333;
      Best Local Similarity   23.6%;   Pred. No. 59;

RESULT 1363
ID   ABP81897 standard; protein; 333 AA.
DE   Human G protein-coupled receptor GPR8 protein SEQ ID NO:279.
PN   WO20026108-A2.
PD   08-AUG-2002.
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
      Query Match   5.9%;   Score 70;   DB 6;   Length 333;
      Best Local Similarity   23.6%;   Pred. No. 59;

RESULT 1364
ID   ABR57245 standard; protein; 333 AA.
DE   Human GPR8 protein SEQ ID NO:84.
PN   WO20030459994-A1.
PD   05-JUN-2003.
PA   (TAKE) TAKEDA CHEM IND LTD.
      Query Match   5.9%;   Score 70;   DB 6;   Length 333;
      Best Local Similarity   23.6%;   Pred. No. 59;

RESULT 1365
ID   ADC22691 standard; protein; 333 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #44.
PN   US6555339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
      Query Match   5.9%;   Score 70;   DB 7;   Length 333;
      Best Local Similarity   23.6%;   Pred. No. 59;

RESULT 1366
ID   ADC22535 standard; protein; 333 AA.
DE   Human G protein-coupled receptor (GPCR) polypeptide #5.
PN   US6555339-B1.
PD   29-APR-2003.
PA   (AREN-) ARENA PHARM INC.
      Query Match   5.9%;   Score 70;   DB 7;   Length 333;
      Best Local Similarity   23.6%;   Pred. No. 59;

RESULT 1367
ID   ADC51793 standard; protein; 333 AA.
DE   Human GPR8, SEQ ID 4.
PN   WO2003057236-A1.
PD   17-JUL-2003.
PA   (FARB) BAYER AG.
      Query Match   5.9%;   Score 70;   DB 7;   Length 333;
      Best Local Similarity   23.6%;   Pred. No. 59;

RESULT 1368
ID   ABR61545 standard; protein; 333 AA.
DE   Human GPR8 receptor polypeptide.
PN   WO2003081234-A2.
PD   02-OCT-2003.
PA   (FARB) BAYER AG.
      Query Match   5.9%;   Score 70;   DB 7;   Length 333;
      Best Local Similarity   23.6%;   Pred. No. 59;

RESULT 1369
ID   ADG41976 standard; protein; 333 AA.
DE   Human GPR8 polypeptide.
PN   JP2003009867-A.
PD   14-JAN-2003.
PA   (TAKE) TAKEDA CHEM IND LTD.
      Query Match   5.9%;   Score 70;   DB 7;   Length 333;
      Best Local Similarity   23.6%;   Pred. No. 59;

RESULT 1370
ID   ADH14008 standard; protein; 333 AA.
DE   Human GPR8.
PN   US2003105292-A1.
PD   05-JUN-2003.
PA   (CHAL/) CHALMERS D T.
      Query Match   5.9%;   Score 70;   DB 7;   Length 333;
      Best Local Similarity   23.6%;   Pred. No. 59;

RESULT 1371
ID   ADH14164 standard; protein; 333 AA.
DE   Mutated human GPR8.
PN   US2003105292-A1.
PD   05-JUN-2003.
PA   (LIAW/) LIAW C W.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.
      Query Match   5.9%;   Score 70;   DB 7;   Length 333;
      Best Local Similarity   23.6%;   Pred. No. 59;

RESULT 1372
ID   ADG12852 standard; protein; 333 AA.
DE   Human wild-type hGPR8 amino acid sequence SEQ ID NO:75.
PN   WO2003097795-A2.
PD   27-NOV-2003.
PA   (NORA-) NORAK BIOSCI INC.
      Query Match   5.9%;   Score 70;   DB 8;   Length 333;
      Best Local Similarity   23.6%;   Pred. No. 59;

RESULT 1373
ID   ADO29700 standard; protein; 333 AA.
DE   Human GPCR GPR8, SEQ ID NO:802.
PN   WO2004040000-A2.
PD   13-MAY-2004.
PA   (PRIM-) PRIMAL INC.
      Query Match   5.9%;   Score 70;   DB 8;   Length 333;
      Best Local Similarity   23.6%;   Pred. No. 59;

RESULT 1374
ID   ADO31044 standard; protein; 333 AA.
DE   Human GPR8 protein SEQ ID NO:73.
PN   WO2004041301-A1.
PD   21-MAY-2004.
PA   (TAKE) TAKEDA CHEM IND LTD.
      Query Match   5.9%;   Score 70;   DB 8;   Length 333;
      Best Local Similarity   23.6%;   Pred. No. 59;

RESULT 1375
ID   ADQ19919 standard; protein; 333 AA.
DE   Human soft tissue sarcoma-upregulated protein - SEQ ID 2738.
PN   WO2004049938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
      Query Match   5.9%;   Score 70;   DB 8;   Length 333;
      Best Local Similarity   23.6%;   Pred. No. 59;

RESULT 1376
ID   ADS14162 standard; protein; 333 AA.
DE   Human GPR8 ligand protein SeqID 73.
PN   WO2004080485-A1.
PD   23-SEP-2004.
PA   (TAKE) TAKEDA CHEM IND LTD.
      Query Match   5.9%;   Score 70;   DB 8;   Length 333;
      Best Local Similarity   23.6%;   Pred. No. 59;

RESULT 1377
ID   ADV24041 standard; protein; 333 AA.
DE   Neuropeptide W antibody associated polypeptide seqid 17.
PN   WO2004106382-A1.
PD   09-DEC-2004.
PA   (TAKE) TAKEDA PHARM CO LTD.
      Query Match   5.9%;   Score 70;   DB 9;   Length 333;
      Best Local Similarity   23.6%;   Pred. No. 59;

RESULT 1378
ID   ADG12854 standard; protein; 347 AA.
DE   Human HA tagged wild-type hGPR8 amino acid sequence SEQ ID NO:77.
PN   WO2003097795-A2.
PD   27-NOV-2003.
PA   (NORA-) NORAK BIOSCI INC.
      Query Match   5.9%;   Score 70;   DB 8;   Length 347;
      Best Local Similarity   23.6%;   Pred. No. 62;

RESULT 1379
ID ABG30839 standard; protein; 364 AA.
DE Human calcium channel protein.
PN WO200252003-A2.
PD 04-JUL-2002.
PA (FRAB) BAYER AG.
Query Match 5.9%; Score 70; DB 5; Length 364;
Best Local Similarity 25.0%; Pred. No. 66;

RESULT 1380
ID ADG12856 standard; protein; 364 AA.
DE Human hGPR8-enhanced receptor amino acid sequence SEQ ID NO:79.
PN WO200309795-A2.
PD 27-NOV-2003.
PA (NORA-) NORAK BIOSCI INC.
Query Match 5.9%; Score 70; DB 8; Length 364;
Best Local Similarity 23.6%; Pred. No. 66;

RESULT 1381
ID AD028778 standard; protein; 364 AA.
DE Human GPR8-enhanced receptor.
PN US200409194\6-A1.
PD 13-MAY-2004.
PA (OAKL/) OAKLEY R H.
PA (BARA/) BARAK L S.
PA (LAPO/) LAPORTE S A.
PA (CARO/) CARON M G.
Query Match 5.9%; Score 70; DB 8; Length 364;
Best Local Similarity 23.6%; Pred. No. 66;

RESULT 1382
ID ADX44597 standard; protein; 364 AA.
DE Enhanced human G-protein coupled receptor 8 - SEQ ID 56.
PN WO200512876-A2.
PD 10-FEB-2005.
PA (NORA-) NORAK BIOSCIENCES INC.
Query Match 5.9%; Score 70; DB 9; Length 364;
Best Local Similarity 23.6%; Pred. No. 66;

RESULT 1383
ID ADY83827 standard; protein; 364 AA.
DE hGPR8-enhanced receptor.
PN WO200502903\5-A2.
PD 31-MAR-2005.
PA (NORA-) NORAK BIOSCIENCES INC.
Query Match 5.9%; Score 70; DB 9; Length 364;
Best Local Similarity 23.6%; Pred. No. 66;

RESULT 1384
ID ADG12858 standard; protein; 378 AA.
DE HA tagged hGPR8-enhanced receptor amino acid sequence SEQ ID NO:81.
PN WO200309795-A2.
PD 27-NOV-2003.
PA (NORA-) NORAK BIOSCI INC.
Query Match 5.9%; Score 70; DB 8; Length 378;
Best Local Similarity 23.6%; Pred. No. 70;

RESULT 1385
ID ADN49121 standard; protein; 388 AA.
DE Mouse oxytocin receptor protein.
PN US200408688\1-A1.
PD 06-MAY-2004.
PA (RAMA/) RAMANATHAN C S.
PA (GOPA/) GOPAL S.
PA (MINT/) MINTIER G A.
PA (FEDE/) FEDER J.
Query Match 5.9%; Score 70; DB 8; Length 388;
Best Local Similarity 24.8%; Pred. No. 73;

RESULT 1386
ID ADC29591 standard; protein; 388 AA.
DE Mouse GPCR OXTR, SEQ ID NO:693.
PN WO200404000\0-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.9%; Score 70; DB 8; Length 388;
Best Local Similarity 24.8%; Pred. No. 73;

RESULT 1387
ID ADA54410 standard; protein; 399 AA.
DE Human protein, SEQ ID 1978.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.9%; Score 70; DB 6; Length 399;
Best Local Similarity 22.9%; Pred. No. 75;

RESULT 1388
ID ABG99947 standard; protein; 399 AA.
DE Human novel polypeptide #60.
PN WO200274961-A1.
PD 26-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 70; DB 6; Length 399;
Best Local Similarity 22.9%; Pred. No. 75;

RESULT 1389
ID ADC96947 standard; protein; 425 AA.
DE E. faecium protein sequence SEQ ID 6574.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70; DB 7; Length 425;
Best Local Similarity 25.9%; Pred. No. 82;

RESULT 1390
ID ADA34110 standard; protein; 470 AA.
DE Acinetobacter baumannii protein #1271.
PN US6562958-B1.
PD 13-MAY-2003.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70; DB 6; Length 470;
Best Local Similarity 23.5%; Pred. No. 95;

RESULT 1391
ID ABM67264 standard; protein; 474 AA.
DE Photorhabdus luminescens protein sequence #361.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70; DB 6; Length 474;
Best Local Similarity 22.9%; Pred. No. 96;

RESULT 1392
ID AAE16787 standard; protein; 475 AA.
DE Human transporter and ion channel-24 (TRICH-24) protein.
PN WO200192304-A2.
PD 06-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.9%; Score 70; DB 5; Length 475;
Best Local Similarity 25.0%; Pred. No. 96;

RESULT 1393
ID ADA89683 standard; protein; 506 AA.
DE Staphylococcus aureus antigenic protein #222.
PN WO200301899-A2.
PD 13-FEB-2003.
PA (UYSH-) UNIV SHEFFIELD.
PA (BIOS-) BIOSYNEXUS INC.
Query Match 5.9%; Score 70; DB 6; Length 506;
Best Local Similarity 25.0%; Pred. No. 1e+02;

RESULT 1394
ID ABM72414 standard; protein; 506 AA.
DE Staphylococcus aureus protein #1654.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 5.9%; Score 70; DB 6; Length 506;
Best Local Similarity 20.1%; Pred. No. 1e+02;

RESULT 1395
ID AAE21176 standard; protein; 540 AA.
DE Human TRICH-20 protein.
PN WO200212340-A2.
PD 14-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.9%; Score 70; DB 5; Length 540;
Best Local Similarity 25.0%; Pred. No. 1.1e+02;

RESULT 1396

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ID   AAM39017 standard; protein; 552 AA.
DE   Human polypeptide SEQ ID NO 2162.
PN   WO200153312-A1.
PD   26-JUL-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match            5.9%;   Score 70;   DB 4;   Length 552;
     Best Local Similarity 25.0%;   Pred. No. 1.2e+02;

RESULT 1397
ID   ABU18262 standard; protein; 602 AA.
DE   Protein encoded by Prokaryotic essential gene #3789.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match            5.9%;   Score 70;   DB 6;   Length 602;
     Best Local Similarity 26.4%;   Pred. No. 1.3e+02;

RESULT 1398
ID   ABU33453 standard; protein; 637 AA.
DE   Protein encoded by Prokaryotic essential gene #18980.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match            5.9%;   Score 70;   DB 6;   Length 637;
     Best Local Similarity 23.1%;   Pred. No. 1.4e+02;

RESULT 1399
ID   AEB39900 standard; protein; 637 AA.
DE   L. pneumophila protein SEQ ID NO 4232.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP ) INST PASTEUR.
     Query Match            5.9%;   Score 70;   DB 9;   Length 637;
     Best Local Similarity 21.4%;   Pred. No. 1.4e+02;

RESULT 1400
ID   AAY91335 standard; protein; 640 AA.
DE   Group B Streptococcus protein sequence SEQ ID NO:68.
PN   WO200006736-A2.
PD   10-FEB-2000.
PA   (MICR-) MICROBIAL TECHNICS LTD.
     Query Match            5.9%;   Score 70;   DB 3;   Length 640;
     Best Local Similarity 22.3%;   Pred. No. 1.5e+02;

RESULT 1401
ID   AEB36499 standard; protein; 647 AA.
DE   L. pneumophila protein SEQ ID NO 831.
PN   WO2005049642-A2.
PD   02-JUN-2005.
PA   (INSP ) INST PASTEUR.
     Query Match            5.9%;   Score 70;   DB 9;   Length 647;
     Best Local Similarity 22.3%;   Pred. No. 1.5e+02;

RESULT 1402
ID   ABM83818 standard; protein; 695 AA.
DE   Human diagnostic and therapeutic protein SEQ ID NO:4067.
PN   WO200423973-A2.
PD   25-MAR-2004.
PA   (INCY-) INCYTE CORP.
     Query Match            5.9%;   Score 70;   DB 8;   Length 695;
     Best Local Similarity 28.6%;   Pred. No. 1.6e+02;

RESULT 1403
ID   ADL04660 standard; protein; 767 AA.
DE   M. catarrhalis protein #426.
PN   US6673910-B1.
PD   06-JAN-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match            5.9%;   Score 70;   DB 8;   Length 767;
     Best Local Similarity 21.3%;   Pred. No. 1.9e+02;

RESULT 1404
ID   AAR53921 standard; protein; 980 AA.
DE   HCV fusion protein corresp. to N-terminal of ORF.
PN   JP06092996-A.
PD   05-APR-1994.
PA   (SHIM/) SHIMOTOYA K.
     Query Match            5.9%;   Score 70;   DB 2;   Length 980;
     Best Local Similarity 24.6%;   Pred. No. 2.6e+02;

RESULT 1405
ID   ADS24062 standard; protein; 1041 AA.
DE   Bacterial polypeptide #13095.
PN   US2003233675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAY/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
     Query Match            5.9%;   Score 70;   DB 8;   Length 1041;
     Best Local Similarity 23.4%;   Pred. No. 2.6e+02;

RESULT 1406
ID   ADU69762 standard; protein; 1049 AA.
DE   S agalactiae hyperimmune serum reactive antigen.seqid 276.
PN   WO2004092242-A2.
PD   18-NOV-2004.
PA   (INTE-) INTERCELL AG.
     Query Match            5.9%;   Score 70;   DB 8;   Length 1049;
     Best Local Similarity 18.8%;   Pred. No. 2.9e+02;

RESULT 1407
ID   ADU69581 standard; protein; 1049 AA.
DE   S agalactiae hyperimmune serum reactive antigen seqid 457.
PN   WO2004092242-A2.
PD   18-NOV-2004.
PA   (INTE-) INTERCELL AG.
     Query Match            5.9%;   Score 70;   DB 8;   Length 1049;
     Best Local Similarity 18.8%;   Pred. No. 2.9e+02;

RESULT 1408
ID   ADU69756 standard; protein; 1049 AA.
DE   S agalactiae hyperimmune serum reactive antigen seqid 451.
PN   WO2004092242-A2.
PD   18-NOV-2004.
PA   (INTE-) INTERCELL AG.
     Query Match            5.9%;   Score 70;   DB 8;   Length 1049;
     Best Local Similarity 18.8%;   Pred. No. 2.9e+02;

RESULT 1409
ID   ADV87847 standard; protein; 1049 AA.
DE   Streptococcus agalactiae protein sequence, SEQ ID 241.
PN   FR2824074-A1.
PD   31-OCT-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
     Query Match            5.9%;   Score 70;   DB 8;   Length 1049;
     Best Local Similarity 18.8%;   Pred. No. 2.9e+02;

RESULT 1410
ID   ADV79100 standard; protein; 1049 AA.
DE   Streptococcus agalactiae protein, SEQ ID 241.
PN   WO200292818-A2.
PD   21-NOV-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
     Query Match            5.9%;   Score 70;   DB 8;   Length 1049;
     Best Local Similarity 18.8%;   Pred. No. 2.9e+02;

RESULT 1411
ID   ADV82666 standard; protein; 1049 AA.
DE   Streptococcus agalactiae protein, SEQ ID 3807.
PN   WO200292818-A2.
PD   21-NOV-2002.
PA   (INSP ) INST PASTEUR.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
     Query Match            5.9%;   Score 70;   DB 8;   Length 1049;
     Best Local Similarity 18.8%;   Pred. No. 2.9e+02;

RESULT 1412
ID   ADV81299 standard; protein; 1049 AA.
DE   Streptococcus agalactiae protein, SEQ ID 2440.
PN   WO200292818-A2.
PD   21-NOV-2002.
PA   (INSP ) INST PASTEUR.
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PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.8%; Score 70; DB 8; Length 1049;
Best Local Similarity 18.8%; Pred. No. 2.9e+02;
RESULT 1413
ID ADV82607 standard; protein; 1049 AA.
DE Streptococcus agalactiae protein, SEQ ID 3748.
PN WO2002092818-A2.
PD 21-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.9%; Score 70; DB 8; Length 1049;
Best Local Similarity 18.8%; Pred. No. 2.9e+02;
RESULT 1414
ID ADP07803 standard; protein; 138 AA.
DE Human secreted protein, seq id 286.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.8%; Score 69.5; DB 8; Length 138;
Best Local Similarity 22.0%; Pred. No. 20;
RESULT 1415
ID ADA33664 standard; protein; 198 AA.
DE Acinetobacter baumannii protein #825.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 198;
Best Local Similarity 23.3%; Pred. No. 33;
RESULT 1416
ID ADB09276 standard; protein; 201 AA.
DE Alloiococcus otitis antigenic protein SEQ ID NO:3216.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 201;
Best Local Similarity 26.0%; Pred. No. 33;
RESULT 1417
ID AEB41646 standard; protein; 201 AA.
DE L. pneumophila protein SEQ ID NO 5978.
PN WO2005049642-A2.
PD 02-JUN-2005.
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.8%; Score 69.5; DB 9; Length 201;
Best Local Similarity 17.6%; Pred. No. 33;
RESULT 1418
ID AAU29449 standard; protein; 210 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #70.
PN WO2001688858-A2.
PD 20-SEP-2001.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 5.8%; Score 69.5; DB 4; Length 210;
Best Local Similarity 20.9%; Pred. No. 35;
RESULT 1419
ID ABG60737 standard; protein; 210 AA.
DE Novel G protein coupled receptor (nGCPR-x) #70.
PN US2005058306-A1.
PD 16-MAY-2002.
PA (VOGE/) VOGELI G.
Query Match 5.8%; Score 69.5; DB 5; Length 210;
Best Local Similarity 20.9%; Pred. No. 35;
RESULT 1420
ID AAU01288 standard; protein; 218 AA.
DE Brassica napus fatty acid desaturase, Fad3C, mutant partial sequence.
PN WO2003125453-A2.
PD 12-APR-2001.
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
Query Match 5.8%; Score 69.5; DB 4; Length 218;
Best Local Similarity 29.3%; Pred. No. 37;
RESULT 1421
ID ADB09278 standard; protein; 247 AA.

DE Alloiococcus otitis antigenic protein SEQ ID NO:3218.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 247;
Best Local Similarity 26.0%; Pred. No. 44;
RESULT 1422
ID ABG66935 standard; protein; 253 AA.
DE Novel G-protein coupled receptor related protein #12.
PN WO2002040539-A2.
PD 23-MAY-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 69.5; DB 5; Length 253;
Best Local Similarity 24.2%; Pred. No. 46;
RESULT 1423
ID ABB62542 standard; protein; 261 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 14418.
PN WO2001711042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.8%; Score 69.5; DB 4; Length 261;
Best Local Similarity 27.7%; Pred. No. 48;
RESULT 1424
ID ABO80446 standard; protein; 270 AA.
DE Pseudomonas aeruginosa polypeptide #12621.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 7; Length 270;
Best Local Similarity 22.1%; Pred. No. 50;
RESULT 1425
ID ADB86076 standard; protein; 296 AA.
DE Streptomyces hygroscopicus ABC transporter.
PN WO2003082909-A1.
PD 09-OCT-2003.
PA (AMHP) WYETH.
Query Match 5.8%; Score 69.5; DB 7; Length 296;
Best Local Similarity 21.0%; Pred. No. 57;
RESULT 1426
ID AAG71524 standard; protein; 308 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1205.
PN WO2001127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
Query Match 5.8%; Score 69.5; DB 4; Length 308;
Best Local Similarity 20.9%; Pred. No. 60;
RESULT 1427
ID ABB44525 standard; protein; 308 AA.
DE Human GPCR3 polypeptide SEQ ID NO 9.
PN WO2001174904-A2.
PD 11-OCT-2001.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 5.8%; Score 69.5; DB 4; Length 308;
Best Local Similarity 20.9%; Pred. No. 60;
RESULT 1428
ID AAU24742 standard; protein; 308 AA.
DE Human olfactory receptor AOLFR242.
PN WO2001168805-A2.
PD 20-SEP-2001.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 69.5; DB 4; Length 308;
Best Local Similarity 20.9%; Pred. No. 60;
RESULT 1429
ID ABP95703 standard; protein; 308 AA.
DE Human GPCR polypeptide SEQ ID NO 216.
PN WO2002016548-A2.
PD 28-FEB-2002.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.8%; Score 69.5; DB 5; Length 308;
Best Local Similarity 20.9%; Pred. No. 60;
RESULT 1430
ID AAU95729 standard; protein; 308 AA.

DE Human olfactory and pheromone G protein-coupled receptor #216.
PN WO20224726-A2.
PD 28-MAR-2002.
PA (CHEM-) CHEMCOM SA.

RESULT 1431
Best Local Similarity 20.9%;   Query Match 5.8%;   Score 69.5;   Pred. No. 60;   DB 5;   Length 308;
ID AAU85362 standard; protein; 308 AA.
DE G-coupled olfactory receptor #223.
PN EP1270724-A2.
PD 02-JAN-2003.
PN WO20198526-A2.
PD 27-DEC-2001.
PA (SENO-) SENOMYX INC.

RESULT 1432
Best Local Similarity 20.9%;   Query Match 5.8%;   Score 69.5;   Pred. No. 60;   DB 5;   Length 308;
ID ADC6633 standard; protein; 308 AA.
DE Human GPCR protein SEQ ID NO.786.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

RESULT 1433
Best Local Similarity 20.9%;   Query Match 5.8%;   Score 69.5;   Pred. No. 60;   DB 7;   Length 308;
ID ABW02126 standard; protein; 308 AA.
DE Human GPCR3 protein.
PN US2003195335-A1.
PD 16-OCT-2003.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (CASM/) CASMAN S.
PA (ALSO/) ALSOBROOK J P.
PA (BURG/) BURGESS C E.
PA (PADI/) PADIGARU M.
PA (TAYL/) TAYLOR S.
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (LILL/) LI L.
PA (SHEN/) SHENOY S.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (STON/) STONE D J.
PA (SMIT/) SMITHSON G.
PA (MACD/) MACDOUGALL J R.

RESULT 1434
Best Local Similarity 20.9%;   Query Match 5.8%;   Score 69.5;   Pred. No. 60;   DB 8;   Length 308;
ID ABR01671 standard; protein; 316 AA.
DE Human G protein coupled receptor SEQ ID 202.
PN WO2003000735-A2.
PD 03-JAN-2003.
PA (DECO-) DECODE GENETICS EHF.

RESULT 1435
Best Local Similarity 20.9%;   Query Match 5.8%;   Score 69.5;   Pred. No. 63;   DB 6;   Length 316;
ID ADU20551 standard; protein; 317 AA.
DE A. thaliana At5g67210 homologue.
PN WO20040092349-A2.
PD 28-OCT-2004.
PA (BADI) BASF PLANT SCI GMBH.

RESULT 1436
Best Local Similarity 33.7%;   Query Match 5.8%;   Score 69.5;   Pred. No. 63;   DB 8;   Length 317;
ID ADU20398 standard; protein; 317 AA.
DE A. thaliana drought tolerance-associated protein At5g67210.
PN WO20040092349-A2.
PD 28-OCT-2004.
PA (BADI) BASF PLANT SCI GMBH.

RESULT 1437
Best Local Similarity 33.7%;   Query Match 5.8%;   Score 69.5;   Pred. No. 63;   DB 6;   Length 317;
ID AAV35360 standard; protein; 321 AA.
DE Chlamydia pneumoniae involved in the virulence process.
PN WO9927105-A2.
PD 03-JUN-1999.
PA (GEST) GENSET.

RESULT 1438
Best Local Similarity 21.4%;   Query Match 5.8%;   Score 69.5;   Pred. No. 64;   DB 2;   Length 321;
ID ADC33485 standard; protein; 321 AA.
DE Yeast ARV1.
PN US6566512-B1.
PD 20-MAY-2003.
PA (UYCO) UNIV COLUMBIA NEW YORK.

RESULT 1439
Best Local Similarity 18.8%;   Query Match 5.8%;   Score 69.5;   Pred. No. 64;   DB 7;   Length 321;
ID ADE37749 standard; protein; 321 AA.
DE Yeast ARV1 (ARE-2 Required for viability).
PN US2003186879-A1.
PD 02-OCT-2003.
PA (UYCO) UNIV COLUMBIA NEW YORK.

RESULT 1440
Best Local Similarity 18.8%;   Query Match 5.8%;   Score 69.5;   Pred. No. 64;   DB 7;   Length 327;
ID AAU53139 standard; protein; 327 AA.
DE Propionibacterium acnes immunogenic protein #14035.
PN WO20018581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.

RESULT 1441
Best Local Similarity 25.5%;   Query Match 5.8%;   Score 69.5;   Pred. No. 66;   DB 4;   Length 327;
ID ABM49658 standard; protein; 327 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #14334.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.

RESULT 1442
Best Local Similarity 25.5%;   Query Match 5.8%;   Score 69.5;   Pred. No. 66;   DB 6;   Length 354;
ID ADH10684 standard; protein; 354 AA.
DE Rat Sprague-Dawley putative GCR polypeptide.
PN WO2003104484-A1.
PD 18-DEC-2003.
PA (META-) METABOLEX INC.

RESULT 1443
Best Local Similarity 22.0%;   Query Match 5.8%;   Score 69.5;   Pred. No. 73;   DB 8;   Length 354;
ID AAY05489 standard; protein; 382 AA.
DE Human EDG-2 protein sequence.
PN WO9919513-A2.
PD 22-APR-1999.
PA (LXRB-) LXR BIOTECHNOLOGY INC.

RESULT 1444
Best Local Similarity 20.2%;   Query Match 5.8%;   Score 69.5;   Pred. No. 81;   DB 2;   Length 382;
ID AAU00302 standard; protein; 382 AA.
DE LPA receptor-related amino acid sequence #1.
PN WO200112838-A2.
PD 22-FEB-2001.
PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.

RESULT 1445
Best Local Similarity 20.2%;   Query Match 5.8%;   Score 69.5;   Pred. No. 81;   DB 4;   Length 382;
ID ABG76099 standard; protein; 382 AA.
DE Human lysophosphatidic acid (LPA) receptor EDG-1.
PN US6485922-B1.
PD 26-NOV-2002.
PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.

RESULT 1446
Best Local Similarity 20.2%;   Query Match 5.8%;   Score 69.5;   Pred. No. 81;   DB 6;   Length 382;
ID ABB47613 standard; protein; 400 AA.
DE Listeria monocytogenes protein #317.
PN WO200177335-A2.

PD   18-OCT-2001.
PA   (INSP) INST PASTEUR.
     Query Match   5.8%;
     Best Local Similarity 22.9%; Score 69.5; DB 5; Length 400;

RESULT 1447
ID   ABU32698 standard; protein; 400 AA.
DE   Protein encoded by Prokaryotic essential gene #18225.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   5.8%;
     Best Local Similarity 22.9%; Score 69.5; DB 6; Length 400;

RESULT 1448
ID   ADL12060 standard; protein; 401 AA.
DE   Drosophila dmTrp1 protein.
PN   WO200302137-A2.
PD   09-JAN-2003.
PA   (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
     Query Match   5.8%;
     Best Local Similarity 20.9%; Score 69.5; DB 7; Length 401;

RESULT 1449
ID   ABB60948 standard; protein; 415 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 9636.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   5.8%;
     Best Local Similarity 20.9%; Score 69.5; DB 4; Length 415;

RESULT 1450
ID   ADL12059 standard; protein; 415 AA.
DE   Drosophila dmTrp1alt2 protein.
PN   WO200302137-A2.
PD   09-JAN-2003.
PA   (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
     Query Match   5.8%;
     Best Local Similarity 20.9%; Score 69.5; DB 7; Length 415;

RESULT 1451
ID   ABB66992 standard; protein; 428 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 27768.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.
     Query Match   5.8%;
     Best Local Similarity 20.9%; Score 69.5; DB 4; Length 428;

RESULT 1452
ID   ADL12058 standard; protein; 428 AA.
DE   Drosophila dmTrp1alt1 protein.
PN   WO200302137-A2.
PD   09-JAN-2003.
PA   (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
     Query Match   5.8%;
     Best Local Similarity 20.9%; Score 69.5; DB 7; Length 428;

RESULT 1453
ID   AAY41284 standard; protein; 444 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 36988.
PN   EP103405-A2.
PD   06-SEP-2000.
PA   (UYVA-) UNIV VANDERBILT.
     Query Match   5.8%;
     Best Local Similarity 23.6%; Score 69.5; DB 2; Length 444;

RESULT 1454
ID   AAG30875 standard; protein; 453 AA.
DE   ci-NT-his fusion protein encoded by plasmid pLJM6-09.
PN   WO995303-A1.
PD   21-OCT-1999.
PA   (UYVA-) UNIV VANDERBILT.
     Query Match   5.8%;
     Best Local Similarity 23.3%; Score 69.5; DB 3; Length 453;

RESULT 1455
ID   ADK47327 standard; protein; 453 AA.
DE   Streptococcus pneumoniae protein, Seq ID No 3842.
PN   US669703-B1.
PD   02-MAR-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   5.8%;
     Best Local Similarity 24.4%; Score 69.5; DB 8; Length 453;

RESULT 1456
ID   ADR95087 standard; protein; 461 AA.
DE   Novel S. pneumoniae protein sequence, SEQ ID 3722.
PN   US680744-B1.
PD   05-OCT-2004.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   5.8%;
     Best Local Similarity 24.4%; Score 69.5; DB 8; Length 461;

RESULT 1457
ID   AEA58957 standard; protein; 461 AA.
DE   Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:3722.
PN   US2005136404-A1.
PD   23-JUN-2005.
PA   (DOUC/) DOUCETTE-STAMM L A.
PA   (BUSH/) BUSH D.
     Query Match   5.8%;
     Best Local Similarity 24.4%; Score 69.5; DB 9; Length 461;

RESULT 1458
ID   AAG30874 standard; protein; 476 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 36987.
PN   EP103405-A2.
PD   06-SEP-2000.
PA   (UYVA-) UNIV VANDERBILT.
     Query Match   5.8%;
     Best Local Similarity 23.3%; Score 69.5; DB 3; Length 476;

RESULT 1459
ID   ADN22349 standard; protein; 477 AA.
DE   Bacterial polypeptide #5002.
PN   US200323675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (GOLD//) GOLDMAN B S.
     Query Match   5.8%;
     Best Local Similarity 21.2%; Score 69.5; DB 8; Length 477;

RESULT 1460
ID   ADS28512 standard; protein; 490 AA.
DE   Bacterial polypeptide #17545.
PN   US200323675-A1.
PD   18-DEC-2003.
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (GOLD//) GOLDMAN B S.
     Query Match   5.8%;
     Best Local Similarity 23.5%; Score 69.5; DB 8; Length 490;

RESULT 1461
ID   AB061637 standard; protein; 494 AA.
DE   Klebsiella pneumoniae polypeptide seqid 8154.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
     Query Match   5.8%;
     Best Local Similarity 22.0%; Score 69.5; DB 7; Length 494;

RESULT 1462
ID   AAY41278 standard; protein; 500 AA.
DE   Fusion protein containing rabbit prostaglandin E2EP3 receptor.
PN   WO995303-A1.
PD   21-OCT-1999.
PA   (UYVA-) UNIV VANDERBILT.
     Query Match   5.8%;
     Best Local Similarity 22.0%; Score 69.5; DB 2; Length 500;

RESULT 1463
ID   AAG30873 standard; protein; 503 AA.
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 36986.
PN   EP103405-A2.
PD   06-SEP-2000.
PA   (UYVA-) UNIV VANDERBILT.
     Query Match   5.8%;
     Best Local Similarity 23.3%; Score 69.5; DB 3; Length 503;

RESULT 1464
ID   AAY92829 standard; protein; 535 AA.
DE   C. pneumoniae CPN100557 processed antigen.
PN   WO20024765-A2.
PD   04-MAY-2000.
PA   (CONN-) CONNAUGHT LAB LTD.
Query Match   5.8%; Score 69.5; DB 3; Length 535;
Best Local Similarity   21.4%; Pred. No. 1.3e+02;

RESULT 1465
ID   ADR13717 standard; protein; 540 AA.
DE   Amidase, SEQ ID 54.
PN   WO20040698848-A2.
PD   19-AUG-2004.
PA   (DIVE-) DIVERSA CORP.
Query Match   5.8%; Score 69.5; DB 8; Length 540;
Best Local Similarity   23.7%; Pred. No. 1.3e+02;

RESULT 1466
ID   AAY92828 standard; protein; 547 AA.
DE   C. pneumoniae CPN100557 antigen.
PN   WO20024765-A2.
PD   04-MAY-2000.
PA   (CONN-) CONNAUGHT LAB LTD.
Query Match   5.8%; Score 69.5; DB 3; Length 547;
Best Local Similarity   21.4%; Pred. No. 1.3e+02;

RESULT 1467
ID   ABU26764 standard; protein; 547 AA.
DE   Protein encoded by Prokaryotic essential gene #12291.
PN   WO20027183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   5.8%; Score 69.5; DB 6; Length 547;
Best Local Similarity   21.4%; Pred. No. 1.3e+02;

RESULT 1468
ID   ABU31940 standard; protein; 551 AA.
DE   Protein encoded by Prokaryotic essential gene #17467.
PN   WO20027183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   5.8%; Score 69.5; DB 6; Length 551;
Best Local Similarity   23.6%; Pred. No. 1.4e+02;

RESULT 1469
ID   AAY01650 standard; protein; 557 AA.
DE   A protein with cation transporting activity.
PN   WO9913072-A1.
PD   18-MAR-1999.
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match   5.8%; Score 69.5; DB 2; Length 557;
Best Local Similarity   23.3%; Pred. No. 1.4e+02;

RESULT 1470
ID   AAY83929 standard; protein; 557 AA.
DE   Human carnitine transporter protein OCTN2.
PN   WO20014210-A1.
PD   16-MAR-2000.
PA   (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match   5.8%; Score 69.5; DB 3; Length 557;
Best Local Similarity   26.3%; Pred. No. 1.4e+02;

RESULT 1471
ID   ABG03029 standard; protein; 557 AA.
DE   Novel human diagnostic protein #3020.
PN   WO20015067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
Query Match   5.8%; Score 69.5; DB 4; Length 557;
Best Local Similarity   26.3%; Pred. No. 1.4e+02;

RESULT 1472
ID   ABB82979 standard; protein; 557 AA.
DE   Human SLC22A related protein-GenBank Identifier No. GI# 3242598.
PN   WO20029053-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
Query Match   5.8%; Score 69.5; DB 6; Length 557;
Best Local Similarity   26.3%; Pred. No. 1.4e+02;

RESULT 1473

ID   ABB82980 standard; protein; 557 AA.
DE   Human SLC22A related protein-GenBank Identifier No. GI# 4507005.
PN   WO20029053-A2.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
Query Match   5.8%; Score 69.5; DB 6; Length 557;
Best Local Similarity   26.3%; Pred. No. 1.4e+02;

RESULT 1474
ID   ABO07242 standard; protein; 557 AA.
DE   Human p53 modifying protein, SEQ ID 202.
PN   WO20299122-A1.
PD   12-DEC-2002.
PA   (EXEL-) EXELIXIS INC.
Query Match   5.8%; Score 69.5; DB 7; Length 557;
Best Local Similarity   26.3%; Pred. No. 1.4e+02;

RESULT 1475
ID   ADE09321 standard; protein; 557 AA.
DE   Novel protein-related contig polypeptide sequence #387.
PN   WO20030541152-A2.
PD   03-JUL-2003.
PA   (HYSE-) HYSEQ INC.
Query Match   5.8%; Score 69.5; DB 7; Length 557;
Best Local Similarity   26.3%; Pred. No. 1.4e+02;

RESULT 1476
ID   ADE09261 standard; protein; 557 AA.
DE   Novel protein-related contig polypeptide sequence #327.
PN   WO20030541152-A2.
PD   03-JUL-2003.
PA   (HYSE-) HYSEQ INC.
Query Match   5.8%; Score 69.5; DB 7; Length 557;
Best Local Similarity   26.3%; Pred. No. 1.4e+02;

RESULT 1477
ID   ADP23817 standard; protein; 557 AA.
DE   PRO polypeptide SEQ ID NO:995.
PN   WO20040411170-A2.
PD   21-MAY-2004.
PA   (GETH) GENENTECH INC.
Query Match   5.8%; Score 69.5; DB 8; Length 557;
Best Local Similarity   26.3%; Pred. No. 1.4e+02;

RESULT 1478
ID   ADY79867 standard; protein; 557 AA.
DE   Amino acid sequence of a human SLC22A5 polypeptide.
PN   WO20050526724-A2.
PD   24-MAR-2005.
PA   (FARB-) BAYER HEALTHCARE AG.
Query Match   5.8%; Score 69.5; DB 9; Length 557;
Best Local Similarity   26.3%; Pred. No. 1.4e+02;

RESULT 1479
ID   ADA34637 standard; protein; 559 AA.
DE   Acinetobacter baumannii protein #1798.
PN   US6562958-B1.
PD   13-MAY-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match   5.8%; Score 69.5; DB 6; Length 559;
Best Local Similarity   26.3%; Pred. No. 1.4e+02;

RESULT 1480
ID   ABO62908 standard; protein; 564 AA.
DE   Klebsiella pneumoniae polypeptide seqid 9425.
PN   US6610836-B1.
PD   26-AUG-2003.
PA   (GENO-) GENOME THERAPEUTICS CORP.
Query Match   5.8%; Score 69.5; DB 7; Length 564;
Best Local Similarity   23.6%; Pred. No. 1.4e+02;

RESULT 1481
ID   ABB89665 standard; protein; 568 AA.
DE   Human polypeptide SEQ ID NO 2041.
PN   WO200190004-A2.
PD   29-NOV-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   5.8%; Score 69.5; DB 5; Length 568;
Best Local Similarity   22.4%; Pred. No. 1.4e+02;

RESULT 1482
ID   ADB65515 standard; protein; 573 AA.

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DE   Human protein encoded by clone TEST12027l790.
PA   (INSP ) INST PASTEUR.
PD   18-OCT-2001.
PN   WO20017735-A2.
DE   Listeria monocytogenes protein #114.
ID   ABB47410 standard; protein; 579 AA.
RESULT 1483
     Best Local Similarity 22.7%;    Score 69.5;  DB 7;   Length 573;
     Query Match            5.8%;    Pred. No. 1.4e+02;
PA   (ELIT-) ELITRA PHARM INC.
PD   03-OCT-2002.
PN   WO200277183-A2.
DE   Protein encoded by Prokaryotic essential gene #18230.
ID   ABU32703 standard; protein; 579 AA.
RESULT 1484
     Best Local Similarity 21.1%;    Score 69.5;  DB 5;   Length 579;
     Query Match            5.8%;    Pred. No. 1.4e+02;
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
PD   13-JUN-2002.
PN   WO20024645-A2.
DE   Hypoxia-regulated protein #108.
ID   ABP65234 standard; protein; 599 AA.
RESULT 1485
     Best Local Similarity 21.1%;    Score 69.5;  DB 6;   Length 579;
     Query Match            5.8%;    Pred. No. 1.4e+02;
PA   (MILL-) MILLENNIUM PHARM INC.
PD   31-JUL-2003.
PN   WO2003061573-A2.
DE   Human GAT1 GABA transporter protein.
ID   AAE38584 standard; protein; 599 AA.
RESULT 1486
     Best Local Similarity 19.6%;    Score 69.5;  DB 7;   Length 599;
     Query Match            5.8%;    Pred. No. 1.5e+02;
PA   (FARB ) BAYER AG.
PD   27-FEB-2003.
PN   WO2003016475-A2.
DE   Human Protein P30531, SEQ ID NO 11697.
ID   ADD46025 standard; protein; 599 AA.
RESULT 1487
     Best Local Similarity 19.6%;    Score 69.5;  DB 7;   Length 599;
     Query Match            5.8%;    Pred. No. 1.5e+02;
PA   (GEHO ) GEN HOSPITAL CORP.
PD   21-OCT-1999.
PN   WO9953033-A1.
DE   CI-77A-TL fusion protein encoded by plasmid pLJM5-42T.
ID   AAY41285 standard; protein; 656 AA.
RESULT 1488
     Best Local Similarity 19.6%;    Score 69.5;  DB 2;   Length 599;
     Query Match            5.8%;    Pred. No. 1.5e+02;
PA   (UVA-) UNIV VANDERBILT.
PD   30-APR-2002.
PN   US6380370-B1.
DE   Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5039.
ID   AAP40194 standard; protein; 660 AA.
RESULT 1489
     Best Local Similarity 23.6%;    Score 69.5;  DB 5;   Length 656;
     Query Match            5.8%;    Pred. No. 1.7e+02;
PA   (GENO-) GENOME THERAPEUTICS CORP.
PD   29-JUL-2004.
PN   US200414773-A1.
DE   Staphylococcus epidermis polypeptide seqid 6545.
ID   ADS07250 standard; protein; 660 AA.
RESULT 1490
     Best Local Similarity 27.2%;    Score 69.5;  DB 5;   Length 660;
     Query Match            5.8%;    Pred. No. 1.7e+02;
PA   (DOUC/) DOUCETTE-STAMM L.
PA   (BUSH/) BUSH D.
     Query Match            5.8%;    Score 69.5;  DB 8;   Length 660;
     Best Local Similarity 27.2%;    Pred. No. 1.7e+02;


RESULT 1491
ID   AAY17390 standard; protein; 663 AA.
DE   Human vesicle membrane protein-like protein 3.
PN   WO9921994-A2.
PD   06-MAY-1999.
PA   (INCY-) INCYTE PHARM INC.
     Query Match            5.8%;    Score 69.5;  DB 2;   Length 663;
     Best Local Similarity 22.0%;    Pred. No. 1.7e+02;
RESULT 1492
ID   ADM83092 standard; protein; 663 AA.
DE   Human vesicle membrane protein (VMP)2.
PN   US2003175787-A1.
PD   18-SEP-2003.
PA   (INCY-) INCYTE CORP.
     Query Match            5.8%;    Score 69.5;  DB 7;   Length 663;
     Best Local Similarity 22.0%;    Pred. No. 1.7e+02;
RESULT 1493
ID   ADJ64317 standard; protein; 663 AA.
DE   Cartilage differentiation inhibiting protein, SEQ ID 12.
PN   WO2004013326-A1.
PD   12-FEB-2004.
PA   (ASAH ) ASAHI KASEI KK.
     Query Match            5.8%;    Score 69.5;  DB 8;   Length 663;
     Best Local Similarity 22.0%;    Pred. No. 1.7e+02;
RESULT 1494
ID   ADQ96536 standard; protein; 663 AA.
DE   T cell activation associated protein #357.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH ) ASAHI KASEI PHARMA CORP.
     Query Match            5.8%;    Score 69.5;  DB 8;   Length 663;
     Best Local Similarity 22.0%;    Pred. No. 1.7e+02;
RESULT 1495
ID   ADY19824 standard; protein; 663 AA.
DE   PRO polypeptide SEQ ID NO 5630.
PN   WO2005016962-A2.
PD   24-FEB-2005.
PA   (GETH ) GENENTECH INC.
     Query Match            5.8%;    Score 69.5;  DB 9;   Length 663;
     Best Local Similarity 22.0%;    Pred. No. 1.7e+02;
RESULT 1496
ID   ADY14394 standard; protein; 663 AA.
DE   PRO polypeptide SEQ ID NO 200.
PN   WO2005016962-A2.
PD   24-FEB-2005.
PA   (GETH ) GENENTECH INC.
     Query Match            5.8%;    Score 69.5;  DB 9;   Length 663;
     Best Local Similarity 22.0%;    Pred. No. 1.7e+02;
RESULT 1497
ID   ADO09827 standard; protein; 681 AA.
DE   Hamster SGLT homologue protein SEQ ID NO:50.
PN   WO2004039405-A1.
PD   13-MAY-2004.
PA   (TAKE ) TAKEDA CHEM IND LTD.
     Query Match            5.8%;    Score 69.5;  DB 8;   Length 681;
     Best Local Similarity 22.0%;    Pred. No. 1.8e+02;
RESULT 1498
ID   ABU41908 standard; protein; 695 AA.
DE   Protein encoded by Prokaryotic essential gene #27435.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
     Query Match            5.8%;    Score 69.5;  DB 8;   Length 695;
     Best Local Similarity 24.5%;    Pred. No. 1.8e+02;
RESULT 1499
ID   ADJ48367 standard; protein; 764 AA.
DE   Maize oil-associated gene protein #26.
PN   US200402525202-A1.
PD   05-FEB-2004.
PA   (LAUR/) LAURIE C C.
PA   (RAVA/) RAVANELLO M.
PA   (SAVA/) SAVAGE T.
PA   (LEDE/) LEDEAUX J R.
     Query Match            5.8%;    Score 69.5;  DB 6;   Length 695;
     Best Local Similarity 24.3%;    Pred. No. 1.9e+02;
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PA   (ROGE/) ROGERS J A.
Query Match   5.8%;   Score 69.5; DB 8;   Length 764;
Best Local Similarity 21.0%;   Pred. No. 2.1e+02;
RESULT 1500
ID   ABU43821 standard; protein; 801 AA.
DE   Protein encoded by Prokaryotic essential gene #29348.
PN   WO200277183-A2.
PD   03-OCT-2002.
PA   (ELIT-) ELITRA PHARM INC.
Query Match   5.8%;   Score 69.5; DB 6;   Length 801;
Best Local Similarity 19.9%;   Pred. No. 2.3e+02;

OM protein - protein search, using sw model

GenCore version 5.1.9
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Run on: October 31, 2006, 02:22:19 ; Search time 52 Seconds
                 (without alignments)
                 393.888 Million cell updates/sec

Title: US-10-063-518-14
Perfect score: 1195
Sequence: 1 MNHLPEDMENALTGSQSSHA..........EAGSEEAEEKQDSEKPLLEL 234

Scoring table:
Searched:

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1500 summaries

Database :
        Issued Patents AA.*
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        6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	669.5	56.0	176	2	US-10-104-047-2567	Sequence 2567, Ap
2	664	55.6	445	1	US-08-691-814B-6	Sequence 6, Appli
3	85.5	7.2	449	1	US-09-949-016-8594	Sequence 8594, Ap
4	82.5	6.9	341	1	US-08-846-762-92	Sequence 92, Appl
5	80.5	6.7	350	2	US-10-226-629A-16	Sequence 16, App
6	80.5	6.7	891	2	US-09-489-039A-9711	Sequence 9711, Ap
7	79.5	6.7	406	2	US-09-171-699-4	Sequence 4, Appl
8	79.5	6.7	406	5	PCT-US94-02107-2	Sequence 2, Appli
9	79.5	6.7	723	2	US-09-976-594-503	Sequence 503, App
10	78.5	6.6	723	2	US-09-270-767-41033	Sequence 41033, A
11	78.5	6.6	221	2	US-09-270-767-56249	Sequence 56249, A
12	78.5	6.6	221	2	US-09-724-653-2	Sequence 2, Appli
13	78.5	6.6	766	2	US-09-724-653-14	Sequence 14, Appl
14	78.5	6.6	766	2	US-09-724-653-15	Sequence 15, Appl
15	78	6.6	228	2	US-09-248-796A-20444	Sequence 20444, A
16	78	6.5	251	2	US-09-270-767-43373	Sequence 43373, A
17	78	6.5	355	2	US-08-833-752-9	Sequence 9, Appli
18	78	6.5	355	2	US-09-938-719-9	Sequence 9, Appli
19	78	6.5	355	2	US-09-939-226B-9	Sequence 9, Appli
20	78	6.5	355	2	US-09-938-703B-9	Sequence 9, Appl
21	77.5	6.5	892	1	US-10-226-629A-15	Sequence 15, Appl
22	77	6.5	353	1	US-08-466-103A-14	Sequence 14, Appl
23	77	6.4	353	2	US-09-280-420-2	Sequence 2, Appli
24	77	6.4	353	2	US-09-479-195-2	Sequence 2, Appli
25	76.5	6.4	435	2	US-09-489-039A-12344	Sequence 12344, A
26	76.5	6.4	494	1	US-08-464-340A-4	Sequence 4, Appli
27	76.5	6.4	494	5	PCT-US94-08449A-4	Sequence 4, Appli
28	76.5	6.4	555	2	US-10-104-047-2011	Sequence 2011, Ap
29	76	6.4	195	2	US-09-134-000C-5992	Sequence 5992, Ap
30	76	6.4	593	2	US-09-720-317A-22	Sequence 22, Appl
31	75.5	6.3	263	2	US-09-583-110-3148	Sequence 3148, Ap
32	75.5	6.3	263	2	US-09-769-787-119	Sequence 119, App
33	75.5	6.3	264	2	US-09-107-433-4877	Sequence 4877, Ap
34	75.5	6.3	352	2	US-09-492-709A-293	Sequence 293, App
35	75.5	6.3	352	2	US-09-248-796A-14258	Sequence 14258, A
36	75.5	6.3	397	2	US-09-721-870-105	Sequence 105, App
37	75.5	6.3	433	1	US-09-721-870-107	Sequence 107, Appl
38	75.5	6.3	471	2	US-08-477-451-20	Sequence 20, Appl
39	75.5	6.3	499	1	US-09-721-870-40	Sequence 40, Appl
40	75	6.3	467	2	US-09-328-352-5465	Sequence 5465, Ap
41	75	6.3	549	2	US-10-104-000C-4375	Sequence 4375, Ap
42	75	6.3	1131	5	US-10-104-047-2866	Sequence 2866, Ap
43	74.5	6.2	355	1	US-08-153-848-28	Sequence 28, Appl
44	74.5	6.2	355	2	US-09-299-843A-28	Sequence 28, Appl
45	74.5	6.2	355	2	US-09-299-843A-32	Sequence 32, Appl
46	74.5	6.2	355	2	US-09-088-337B-28	Sequence 28, Appl
47	74.5	6.2	355	2	US-09-088-337B-32	Sequence 32, Appl
48	74.5	6.2	355	5	US-09-170-496D-130	Sequence 130, App
49	74.5	6.2	355	2	US-09-170-496D-232	Sequence 232, App
50	74.5	6.2	355	2	US-08-917-254-68	Sequence 68, Appl
51	74.5	6.2	355	5	PCT-US93-11153-28	Sequence 28, Appl
52	74.5	6.2	355	5	PCT-US93-11153-32	Sequence 32, Appl
53	74	6.2	350	1	US-08-466-103A-12	Sequence 12, Appl
54	74.5	6.2	471	2	US-09-032-742-2	Sequence 2, Appl
55	74.5	6.2	471	2	US-09-032-742-11	Sequence 11, Appl
56	74.5	6.2	471	2	US-09-032-742-14	Sequence 14, Appl
57	74.5	6.2	471	2	US-09-032-742-17	Sequence 17, Appl
58	74.5	6.2	471	2	US-09-145-864-4	Sequence 4, Appli
59	74.5	6.2	471	2	US-09-145-864-4	Sequence 4, Appli
60	74.5	6.2	940	2	US-09-328-352-8165	Sequence 8165, Ap
61	74	6.2	154	2	US-09-543-681A-7579	Sequence 7579, Ap
62	74	6.2	332	2	US-09-107-433-2662	Sequence 2662, Ap
63	74	6.2	350	1	US-08-466-103A-12	Sequence 12, Appl
64	74	6.2	680	5	US-09-248-796A-15089	Sequence 15089, A
65	73.5	6.2	312	2	US-09-543-681A-6267	Sequence 6267, Ap
66	73.5	6.2	400	2	US-09-902-540-11488	Sequence 11488, A
67	73.5	6.2	3033	1	US-07-925-695-9	Sequence 9, Appli
68	73	6.2	199	2	US-09-107-532A-6773	Sequence 6773, Ap
69	73	6.1	272	2	US-09-107-532A-6773	Sequence 6773, Ap
70	73	6.1	364	2	US-09-903-456-75	Sequence 75, Appl
71	73	6.1	364	2	US-09-077-675A-16	Sequence 16, Appl
72	73	6.1	364	2	US-09-077-674-16	Sequence 16, Appl
73	73	6.1	364	2	US-09-762-661A-6	Sequence 6, Appli
74	73	6.1	364	2	US-09-743-475-3	Sequence 3, Appli
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76	73	6.1	377	2	US-08-936-165A-533	Sequence 533, App
77	73	6.1	494	2	US-09-949-016-7475	Sequence 7475, Ap
78	73	6.1	501	2	US-09-489-039A-9817	Sequence 9817, Ap
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337	68	5.7	472	2	US-08-716-873-36	Sequence 36, Appl
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358	68	5.7	727	2	US-08-484-840-4	Sequence 4, Appli
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601	65.5	5.5	1226	1	US-08-218-265-12	Sequence 12, Appl
602	65.5	5.5	1226	2	US-08-521-872-12	Sequence 12, Appl
603	65.5	5.5	1226	2	US-08-590-399-12	Sequence 12, Appl
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605	65.5	5.5	1410	2	US-09-037-188-4	Sequence 4, Appli
606	65.5	5.5	1410	2	US-09-285-310-4	Sequence 4, Appli
607	65.5	5.5	1427	2	US-09-753-385-4	Sequence 4, Appli
608	65	5.4	1427	2	US-09-487-558B-354	Sequence 354, App
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614	65	5.4	181	2	US-09-126-640-10	Sequence 10, Appl
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619	65	5.4	182	2	US-09-485-486-8	Sequence 8, Appli
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622	65	5.4	223	2	US-09-949-016-8160	Sequence 8160, Ap
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677	64.5	5.4	346	2	US-08-830-230A-684	Sequence 684, App
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679	64.5	5.4	373	2	US-09-830-230A-683	Sequence 683, App
680	64.5	5.4	393	2	US-09-270-767-42317	Sequence 42317, A
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742	64.5	5.4	351	2	US-09-688-988-28	Sequence 28, Appl
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769	63.5	5.4	555	2	US-09-134-000C-5066	Sequence 5066, Ap
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845	63.5	5.3	489	2	US-09-997-333-138	Sequence 138, App
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853	63.5	5.3	489	3	US-09-989-293A-138	Sequence 138, App
854	63.5	5.3	518	2	US-09-543-681A-4949	Sequence 4949, Ap
855	63.5	5.3	568	2	US-09-469-200E-10	Sequence 10, Appl
856	63.5	5.3	568	1	US-09-107-532A-5495	Sequence 5495, Ap
857	63.5	5.3	759	2	US-08-637-759B-89	Sequence 89, Appl
858	63.5	5.3	759	2	US-08-871-355A-89	Sequence 89, Appl
859	63.5	5.3	759	2	US-09-201-945-89	Sequence 89, Appl
860	63.5	5.3	759	2	US-09-714-602-89	Sequence 89, Appl
861	63.5	5.3	866	2	US-09-997-514-138	Sequence 138, App
862	63.5	5.3	866	2	US-09-989-728-138	Sequence 138, App
863	63.5	5.3	979	3	US-09-385-752-1	Sequence 1, Appli
864	63.5	5.3	2080	2	US-10-104-047-2446	Sequence 2446, Ap
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868	63.5	5.3	197	2	US-09-198-452A-403	Sequence 403, App
869	63.5	5.3	218	2	US-09-134-000C-4489	Sequence 4489, Ap
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875	63.5	5.3	259	2	US-09-456-455A-3	Sequence 3, Appli
876	63.5	5.3	259	2	US-10-080-960-25	Sequence 25, Appl
877	63.5	5.3	264	2	US-09-270-767-41787	Sequence 41787, A
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879	63.5	5.3	299	2	US-09-107-532A-5499	Sequence 5499, Ap
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883	63.5	5.3	361	2	US-09-685-945B-4	Sequence 4, Appli
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885	63.5	5.3	365	2	US-09-685-945B-2	Sequence 2, Appli
886	63.5	5.3	366	2	US-09-107-433-5158	Sequence 5158, Ap
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889	63.5	5.3	370	2	US-09-799-955-3	Sequence 3, Appli
890	63.5	5.3	370	2	US-09-799-955-2	Sequence 2, Appli
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893	63.5	5.3	388	2	US-09-940-921B-7	Sequence 7, Appli
894	63.5	5.3	415	2	US-09-482-746-13	Sequence 13, Appl
895	63.5	5.3	415	2	US-09-580-734-13	Sequence 13, Appl
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897	63.5	5.3	415	2	US-09-191-724-13	Sequence 13, Appl
898	63.5	5.3	422	2	US-09-799-978-22	Sequence 22, Appl
899	63.5	5.3	431	2	US-09-625-188-12	Sequence 12, Appl
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907	63	5.3	508	2	US-10-314-048A-16	Sequence 16, Appl
908	63	5.3	508	2	US-10-314-048A-92	Sequence 92, Appl
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922	63	5.3	1027	2	US-09-902-540-11750	Sequence 11750, A
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928	62.5	5.3	136	2	US-09-270-767-36009	Sequence 36009, A
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935	62.5	5.2	191	2	US-09-989-726-287	Sequence 287, App
936	62.5	5.2	197	3	US-09-997-349-287	Sequence 287, App
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938	62.5	5.2	200	2	US-09-949-349-287	Sequence 287, App
939	62.5	5.2	214	3	US-09-248-796A-15088	Sequence 15088, A
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942	62.5	5.2	255	2	US-09-991-181-287	Sequence 287, App
943	62.5	5.2	255	2	US-09-997-333-287	Sequence 287, App
944	62.5	5.2	255	2	US-09-992-598-287	Sequence 287, App
945	62.5	5.2	255	2	US-09-989-735-287	Sequence 287, App
946	62.5	5.2	255	3	US-09-997-514-287	Sequence 287, App
947	62.5	5.2	255	3	US-09-989-728-287	Sequence 287, App
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965	62.5	5.2	353	2	US-09-949-016-8077	Sequence 8077, Ap
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967	62.5	5.2	367	2	US-09-830-807-26	Sequence 26, Appl
968	62.5	5.2	383	2	US-09-330-235-8	Sequence 8, Appli
969	62.5	5.2	383	5	PCT-US94-01321-2	Sequence 2, Appli
970	62.5	5.2	383	2	US-09-489-039A-7223	Sequence 7223, Ap
971	62.5	5.2	434	2	US-09-198-452A-434	Sequence 434, App
972	62.5	5.2	434	2	US-09-489-039A-434	Sequence 434, App
973	62.5	5.2	439	2	US-09-248-796A-13336	Sequence 13336, A
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992	62.5	5.2	541	2	US-09-713-794-19	Sequence 19, Appl
993	62.5	5.2	541	2	US-09-713-794-20	Sequence 20, Appl
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997	62.5	5.2	578	2	US-09-134-000C-6690	Sequence 6690, Ap
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1040	62.5	5.2	360	1	US-08-202-056-7	Sequence 7, Appli
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1053	62	5.2	413	2	US-09-107-433-2887	Sequence 2887, Ap
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1055	62	5.2	414	2	US-09-438-185A-396	Sequence 396, Appl
1056	62	5.2	415	2	US-09-799-978-28	Sequence 28, Appl
1057	62	5.2	417	2	US-09-710-278-950	Sequence 950, App
1058	62	5.2	432	2	US-09-605-703B-1244	Sequence 1244, Ap
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1089	62	5.2	706	2	US-09-668-650-6	Sequence 6, Appli
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1095	62	5.2	1186	2	US-09-001-982-6	Sequence 6, Appli
1096	61.5	5.2	1186	2	US-09-668-650-6	Sequence 6, Appli
1097	61.5	5.2	1267	2	US-09-543-681A-6130	Sequence 6130, Ap
1098	61.5	5.1	1985	2	US-09-495-714C-6	Sequence 6, Appli
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1263	61	5.1	3011	2	US-10-104-966-1	Sequence 1, Appli
1264	61	5.1	3011	2	US-09-952-572-9	Sequence 9, Appli
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1266	61	5.1	3011	2	US-10-259-275-20	Sequence 20, Appli
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1289	60.5	5.1	205	2	PCT-US95-09927-9	Sequence 9, Appli
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1308	60.5	5.1	342	2	US-09-852-156-2	Sequence 2, Appli
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1334	60.5	5.1	487	2	US-10-09-317-8	Sequence 8, Appli
1335	60.5	5.1	489	2	US-09-986-536-2	Sequence 2, Appli
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1357	60.5	5.1	865	2	US-09-612-204B-24	Sequence 24, Appl
1358	60.5	5.1	1064	2	US-09-248-796A-16640	Sequence 16640, A
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1360	60.5	5.1	1323	2	US-09-248-796A-46728	Sequence 46728, A
1361	60.5	5.1	1912	2	US-09-913-832A-2	Sequence 2, Appli
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1363	60.5	5.1	1912	2	US-08-513-707-22	Sequence 22, Appl
1364	60.5	5.1	5032	2	US-09-538-092-979	Sequence 979, App
1365	60.5	5.1	136	2	US-09-158-707-22	Sequence 22, Appl
1366	60.5	5.1	136	2	US-09-270-767-317761	Sequence 3161, A
1367	60	5.1	162	2	US-09-134-000C-4993	Sequence 4993, Ap
1368	60	5.0	177	2	US-09-492-308A-23	Sequence 23, Appl
1369	60	5.0	189	2	US-09-270-767-47558	Sequence 47558, A
1370	60	5.0	189	2	US-09-270-767-32341	Sequence 32341, A
1371	60	5.0	189	2	US-09-270-767-3240	Sequence 3240, Ap
1372	60	5.0	191	2	US-09-107-433-3384	Sequence 3384, Ap
1373	60	5.0	199	2	US-09-107-433-3384	Sequence 3384, Ap
1374	60	5.0	204	2	US-09-710-279-3240	Sequence 3240, Ap
1375	60	5.0	206	2	US-08-513-974B-27	Sequence 27, Appl
1376	60	5.0	206	2	US-08-776-971-22	Sequence 22, Appl
1377	60	5.0	206	2	US-08-513-974B-27	Sequence 27, Appl
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1379	60	5.0	223	2	US-09-461-436B-27	Sequence 27, Appl
1380	60	5.0	223	2	US-09-489-039A-11059	Sequence 11059, A
1381	60	5.0	223	2	US-09-513-974B-315	Sequence 315, App
1382	60	5.0	223	2	US-08-513-974B-364	Sequence 364, App
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1421	60	5.0	382	2	US-09-134-001C-4483	Sequence 4483, Ap
1422	60	5.0	387	2	US-09-902-853-6	Sequence 6, Appli
1423	60	5.0	397	1	US-08-990-379-8	Sequence 8, Appli
1424	60	5.0	416	2	US-09-583-110-2732	Sequence 2732, Ap
1425	60	5.0	416	2	US-10-140-372-4	Sequence 4, Appli
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1428	60	5.0	419	2	US-08-385-186-4	Sequence 4, Appli
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1431	60	5.0	420	2	US-09-799-978-42	Sequence 42, Appli
1432	60	5.0	421	2	US-09-543-681A-7791	Sequence 7791, Ap
1433	60	5.0	422	2	US-09-540-236-2283	Sequence 2283, Ap
1434	60	5.0	440	2	US-09-949-016-10558	Sequence 10558, A
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1437	60	5.0	467	2	US-09-690-359-28	Sequence 28, Appl
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1439	60	5.0	478	1	US-10-104-047-2898	Sequence 2898, Ap
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1450	60	5.0	590	2	US-09-052-753B-2	Sequence 2, Appli
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1455	60	5.0	630	2	US-09-602-787A-548	Sequence 548, App
1456	60	5.0	639	2	US-09-134-001C-5661	Sequence 5661, Ap
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1460	60	5.0	734	2	US-09-585-858-9	Sequence 9, Appli
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1464	60	5.0	797	2	US-09-942-016-6657	Sequence 6657, Ap
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1467	60	5.0	1068	2	US-09-481-558B-242	Sequence 242, Appl
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1469	60	5.0	1156	2	US-09-198-452A-171	Sequence 171, App
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1480	60	5.0	1447	2	US-09-754-032-19	Sequence 19, Appl
1481	60	5.0	1447	2	US-08-916-140-19	Sequence 19, Appl
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1485	60	5.0	1659	2	US-09-487-558B-118	Sequence 118, App
1486	60	5.0	1681	2	US-09-920-653B-3	Sequence 3, Appli
1487	60	5.0	2235	2	US-09-032-438C-6	Sequence 6, Appli
1488	60	5.0	2273	2	US-09-032-438C-3	Sequence 3, Appli
1489	60	5.0	2940	2	US-10-226-629A-13	Sequence 13, Appl
1490	60	5.0	3011	1	US-08-453-552-2	Sequence 2, Appli
1491	60	5.0	3011	1	US-08-710-637-2	Sequence 2, Appli
1492	60	5.0	3011	5	PCT-US93-00907-2	Sequence 2, Appli
1493	60	5.0	3033	3	US-10-009-011-4	Sequence 4, Appli
1494	59.5	5.0	151	3	US-09-328-352-4208	Sequence 4208, Ap
1495	59.5	5.0	159	2	US-09-248-796A-27840	Sequence 27840, A
1496	59.5	5.0	159	2	US-09-270-767-36990	Sequence 36990, A
1497	59.5	5.0	161	2	US-09-270-767-52207	Sequence 52207, A
1498	59.5	5.0	195	2	US-08-467-822-44	Sequence 44, Appl
1499	59.5	5.0	195	1	US-08-211-312-3	Sequence 3, Appli
1500	59.5	5.0	195	2	US-08-472-285-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-104-047-2567
Sequence 2567, Application US/10104047
Patent No. 6943241
GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 694324le1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2567
;   LENGTH: 176
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-104-047-2567

Query Match   56.0%; Score 669.5; DB 2; Length 176;
Best Local Similarity   87.5%; Pred. No. 4.3e-69;
Matches 133; Conservative   6; Mismatches 12; Indels   1; Gaps   1;

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RESULT 2
US-08-691-814B-6
; Sequence 6, Application US/08691814B
; Patent No. 5981218
; GENERAL INFORMATION:
; APPLICANT: Rio, Marie-Christine
; APPLICANT: Tomasetto, Catherine
; APPLICANT: Basset, Paul
; APPLICANT: Byrne, Jennifer
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
; TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave, NW, Suite 600
; CITY: Washington
; STATE: DC

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COUNTRY: USA
   ZIP: 20005-3934
COMPUTER READABLE FORM:
   MEDIUM TYPE: Floppy disk
   COMPUTER: IBM PC compatible
   OPERATING SYSTEM: PC-DOS/MS-DOS
   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
   APPLICATION NUMBER: US/08/691,814B
   FILING DATE: 31-JUL-1996
   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
   APPLICATION NUMBER: US 60/002,183
   FILING DATE: 09-AUG-1995
ATTORNEY/AGENT INFORMATION:
   NAME: Steffe, Eric K.
   REGISTRATION NUMBER: 36,688
   REFERENCE/DOCKET NUMBER: 1383.0090001
TELECOMMUNICATION INFORMATION:
   TELEPHONE: 202-371-2600
   TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 6:
   SEQUENCE CHARACTERISTICS:
   LENGTH: 445 amino acids
   TYPE: amino acid
   TOPOLOGY: linear
   MOLECULE TYPE: protein
US-08-691-814B-6

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Best Local Similarity   56.2%;  Pred. No. 6.9e-68;
Matches  135;  Conservative  38;  Mismatches  45;  Indels  22;  Gaps  5;

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RESULT 3
US-09-949-016-8594
Sequence 8594, Application US/0994016
Patent No. 6812339
GENERAL INFORMATION:
   APPLICANT: VENTER, J. Craig et al.
   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
      WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
   FILE REFERENCE: CL001307
   CURRENT APPLICATION NUMBER: US/09/949,016
   CURRENT FILING DATE: 2000-04-14
   PRIOR APPLICATION NUMBER: 60/241,755
   PRIOR FILING DATE: 2000-10-20
   PRIOR APPLICATION NUMBER: 60/237,768
   PRIOR FILING DATE: 2000-10-03
   PRIOR APPLICATION NUMBER: 60/231,498
   PRIOR FILING DATE: 2000-09-08
   NUMBER OF SEQ ID NOS: 207012
   SOFTWARE: FastSEQ for Windows Version 4.0
   SEQ ID NO 8594
   LENGTH: 449
   TYPE: PRT
   ORGANISM: Human


US-09-949-016-8594

Query Match          7.2%;  Score  85.5;  DB 2;  Length 449;
Best Local Similarity   25.5%;  Pred. No. 0.49;
Matches   38;  Conservative  18;  Mismatches  46;  Indels  47;  Gaps  8;

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Qy  109 KVLILAYAVCRLRHWWAIALTTAVTSAFLLLAKVILSKLFSQGAFGYVLPIISFIL----- 163
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Qy  164 ------AWIETWFLDFKVLPQEAEEENR 185
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RESULT 4
US-08-846-762-92
Sequence 92, Application US/0884676A
Patent No. 5994072
GENERAL INFORMATION:
   APPLICANT: Lam, Joseph S.
   APPLICANT: Burrows, Lori
   APPLICANT: Charter, Deborah
   APPLICANT: de Kievit, Teresa
   TITLE OF INVENTION: No. 5994072el Proteins Involved in the Synthesis and Assembly
   TITLE OF INVENTION: of O-Antigen in Pseudomonas Aeruginosa
   FILE REFERENCE: 6580-089
   CURRENT APPLICATION NUMBER: US/08/846,762A
   CURRENT FILING DATE: 1997-04-30
   NUMBER OF SEQ ID NOS: 100
   SOFTWARE: Patentin Ver. 2.0
   SEQ ID NO 92
   LENGTH: 341
   TYPE: PRT
   ORGANISM: Pseudomonas aeruginosa


US-08-846-762-92

Query Match          6.9%;  Score  82.5;  DB 1;  Length 341;
Best Local Similarity   24.0%;  Pred. No. 0.74;
Matches   31;  Conservative  20;  Mismatches  51;  Indels  27;  Gaps  4;

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Qy  107 RFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWI 166
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Db  326 PLIYIDYKL 334

RESULT 5
US-09-489-039A-9711
Sequence 9711, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
   APPLICANT: Gary Breton et. al
   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
   TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
   FILE REFERENCE: 2709.2004001
   CURRENT APPLICATION NUMBER: US/09/489,039A
   CURRENT FILING DATE: 2000-01-27
   PRIOR APPLICATION NUMBER: 60/117,747
   PRIOR FILING DATE: 1999-01-29
   NUMBER OF SEQ ID NOS: 14342
   SEQ ID NO 9711
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; LENGTH: 350
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
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US-09-489-039A-9711
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Matches  21; Conservative  15; Mismatches  21; Indels  9; Gaps  3;
Best Local Similarity  31.8%; Pred. No. 1.3;
Query Match  6.7%; Score 80.5; DB 2; Length 350;

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RESULT 6
US-10-226-629A-16
; Sequence 16, Application US/10226629A
; Patent No. 6960431
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection
; FILE REFERENCE: 5006.01
; CURRENT APPLICATION NUMBER: US/10/226,629A
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,182
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 736
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 891
; TYPE: PRT
; ORGANISM: Vaccinia virus
US-10-226-629A-16

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Matches  38; Conservative  36; Mismatches  70; Indels  19; Gaps  7;
Best Local Similarity  23.3%; Pred. No. 4.9;
Query Match  6.7%; Score 80.5; DB 2; Length 891;

Qy    7 DMENALTGSQSSHASLRNIHSINPTQLMAR-IESYEGREKKGISDVRRTFCLFVTFDLLF 65
Db  717 NMTNEIT--DMINASLKNTISKDNNMLVSQALNSVANRSKQKIGDLRQSSCKMALLFKNL 774

Qy   66 VTLLWIIELNVNGGIENTLEKEVMQ-YDYY-----SSYFDIFLLAVFRFKVLILAYAVCR 119
Db  775 ATSIYTIERIFNAKVGDDVKASMLEKYKVFTDISMSLYKDLIAMENLKAMLYIIRRSGCR 834

Qy  120 LRHWAIALTT--AVTSAFLLAKVILSKL-----FSVPAFGYV 155
Db  835 IDD--AQITDDLVKSYSLIRPKILSMINYYNEMSRGYFEHM 874
```

RESULT 7
US-09-171-699-4
; Sequence 4, Application US/09171699
; Patent No. 6443389
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of, Anatomy & Biology
; APPLICANT: Gonczol, Eva
; APPLICANT: Berencsi, Klara
; APPLICANT: Kari, Csaba
; TITLE OF INVENTION: No. 6443389el Cytomegalovirus DNA Constructs and Uses Therefor
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Center, P.O. Box 457

; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/171,699
; FILING DATE: 19-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/015,717
; FILING DATE: 23-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kodroff, Cathy A.
; REGISTRATION NUMBER: 33,980
; REFERENCE/DOCKET NUMBER: WST66APCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-171-699-4

```
Matches  52; Conservative  36; Mismatches  67; Indels  115; Gaps  12;
Best Local Similarity  19.3%; Pred. No. 2.1;
Query Match  6.7%; Score 79.5; DB 2; Length 406;

Qy   14 GSQSSHASLRNIHSINPTQLMARIESY-----------EGREKKGISDVRRTFCLFVTFVTL 68
Db  142 GCSQAWALQNLPQCSPDEIMAYAQKIFKILDEERDK----------------VLTHIDHIFMDI 190

Qy   69 LWIIELNVNGGIENTLEKEVMQYDY-----------YSSYFDIFLLAVFRFKVLILAYAVCRL 120
Db  191 L-------------TTCVETMCNEYKVTSDACMWTMYGGISLLSEF------CRV 226

Qy  121 RHWAIALTTAVTSAFLLAK----------------------VLLSKLFSQGAFGYVL---- 156
Db  227 LSCTVLEETSV-----MLAKRPLITKPEVISVMKRIEEICMKVPAQ---YILGADPLR 277

Qy  157 --PIISFILAWIETWFLDFKVLPQEAEENRLLIVQDASERAALIPGGLSDGQFYSPPE 213
Db  278 VCSPSVD-------DLRAIAEESDEEEAIVAYTLATR-----GASSSDSLVSPPE 320

Qy  214 S---------EAGSEEAEEKQDSEK 229
Db  321 SPVPATIPLSSVIVAENSDQEESEQSDEEE 350
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RESULT 8
PCT-US94-02107-2
; Sequence 2, Application PCT/US9402107
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of, Anatomy and Biology
; TITLE OF INVENTION: Recombinant Cytomegalovirus Vaccine
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: PCT/US94/02107
  FILING DATE:
  CLASSIFICATION:
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/017,130
  FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
  NAME: Bak, Mary E.
  REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST6BPCT
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 215-540-9200
  TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 2:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 406 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
  MOLECULE TYPE: protein

PCT-US94-02107-2

Query Match 6.7%; Score 79.5; DB 5; Length 406;
Best Local Similarity 19.3%; Pred. No 2.1;
Matches 52; Conservative 36; Mismatches 67; Indels 115; Gaps 12;

```
Qy   14 GSQQSHASLRNHSINPTQLMARIESY------EGREKKGISDVRRTFCLFVTEPLLFVTL  68
Db  142 GCSQAMALQNLPQCSPDEIMAYAQKIFKILDEERDK------------VLTHIDHIFMDI 190

Qy   69 LWIELNVNGGIENTLEKEVMQYDY------YSSYFDIFLLAVFRKVLILAYAVCRL     120
Db  191 L------TTCVETMCNEYKVTSDACMMTMYGGISLLSEF------------CRV       226

Qy  121 RHWWAIALTTAVTSAFLLAK------VILSKLFSQGAFGYVL------             156
Db  227 LSCYVLEETSV----MLAKRPLITKPEVISVMKRRIEEICMKVFAQ----YILGADPLR 277

Qy  157 ---PIISFILAWIETWFLDFKVLPQEAAEENRLLIVQDASERAALIPGGLSDGQFYSPPE 213
Db  278 VCSPSVD------DLRAIAEESDEEEAIVAYTLATR------GASSSDSLVSPPE      320

Qy  214 S------EAGSEEAEEKQDSEK                                       229
Db  321 SPVPATIPLSSVIVAENSDQEESQSDEEE                               350
```

RESULT 9
US-09-976-594-503
Sequence 503, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
  APPLICANT: Furness, Michael
  APPLICANT: Buchbinder, Jenny
  TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
  FILE REFERENCE: PA-0041 US
  CURRENT APPLICATION NUMBER: US/09/976,594
  CURRENT FILING DATE: 2001-10-12
  PRIOR APPLICATION NUMBER: 60/240,409
  PRIOR FILING DATE: 2000-10-12
  NUMBER OF SEQ ID NOS: 1143
  SOFTWARE: PERL Program
  SEQ ID NO 503
  LENGTH: 723
  TYPE: PRT
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: misc_feature
  OTHER INFORMATION: Incyte ID No. 6673549 2246292CD1
US-09-976-594-503

Query Match 6.7%; Score 79.5; DB 2; Length 723;
Best Local Similarity 18.0%; Pred. No. 4.8;
Matches 34; Conservative 40; Mismatches 58; Indels 57; Gaps 8;

```
Qy   58 FVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRKVLI------ 112
Db   13 FMSVDICVTTAIVIF----SHLDRSLLEDIRHFNIFDSVLDIWAACLYRSCLLGATIG   67

Qy  113 ---LAYAVCRLR-HWWAIALTTAVTSAFLLAKVILSKLFSQ------------GAFGY   154
Db   68 VAKNSALGPRRLRASWLVISLVCLFVGIYAMVKLL----LFSEVRRPIRDPWFWALFVWTY 124

Qy  155 VLPIISFILAWIETWFLDFKVLPQEAAEENRLLIVQDASERAALIPGGLSDGQFY----- 209
Db  125 ISLGASFLLMWL------------------LSTVRPGTQ-ALEPGAATEAEGFPGSGR  163

Qy  210 SPPESEAGS                                                    218
Db  164 PPPEQASGA                                                    172
```

RESULT 10
US-09-270-767-41033
Sequence 41033, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
  APPLICANT: Homburger et al.
  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
  FILE REFERENCE: 7326-094
  CURRENT APPLICATION NUMBER: US/09/270,767
  CURRENT FILING DATE: 1999-03-17
  NUMBER OF SEQ ID NOS: 62517
  SOFTWARE: PatentIn Ver. 2.0
  SEQ ID NO 41033
  LENGTH: 221
  TYPE: PRT
  ORGANISM: Drosophila melanogaster
  FEATURE:
  OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41033

Query Match 6.6%; Score 78.5; DB 2; Length 221;
Best Local Similarity 22.5%; Pred. No. 1.2;
Matches 38; Conservative 33; Mismatches 73; Indels 25; Gaps 7;

```
Qy   56 CLFVTFDL---LFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRKVLI  112
Db   17 CIYIYSSMDQFLFIILILLLTCLSFVEXYLFVNILLXIDNYIGNXXNVFLFFLLPQXII   76

Qy  113 LAYAVCRLRHWWAIALTT--AVTSAFLLAKVILSKLFSQGAFGYVL-PIISFILAWIETW 169
Db   77 VVFPCCSFCTTYQLIQGTVNSINFRNLKNLSLT------LGFLISPPISIHFSYLPHY   129

Qy  170 FLDFKVLPQEAAEENRLL-------IVQDASERAAL--IPGGLSDGQF             208
Db  130 LVNNSVLHLKNVXIQEFLDXVVKCFFILRASFRPCLKDIPNGL--GQF             176
```

RESULT 11
US-09-270-767-56249
Sequence 56249, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
  APPLICANT: Homburger et al.
  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
  FILE REFERENCE: 7326-094
  CURRENT APPLICATION NUMBER: US/09/270,767
  CURRENT FILING DATE: 1999-03-17
  NUMBER OF SEQ ID NOS: 62517
  SOFTWARE: PatentIn Ver. 2.0
  SEQ ID NO 56249
  LENGTH: 221

```
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56249

Query Match            6.6%;   Score 78.5;   DB 2;   Length 221;
Best Local Similarity  22.5%;  Pred. No. 1.2;
Matches  38;   Conservative  33;   Mismatches  73;  Indels  25;  Gaps  7;

Qy   56 CLFVTFDL---LFVTLLWIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRKVLI 112
            |::|  :|                  :::|              ::|:|||
Db   17 CIVIYSSMDQFLFIIILILLILLTCLSFVEXYLFVNILXIDNYIGNXNVFLFFLLLFQXII 76

Qy  113 LAYAVCRLRHWWAIALTT--AVTSAFLLAKVILSKLFSQGAFGYVL-PIISFILAWIETW 169
            ::  ||                   |::|  :    : :::  :::|||||||
Db   77 VVYFCCSFCTTYQLIQGTYNSINFRFNLKNLSLT------LGFLISPPISIHFSYLPHY 129

Qy  170 FLDFKVLPQEAEEENRLL------IVQDASERAAL-IPGGLSDGQF 208
            ||  :                  : :  | | ||||   :
Db  130 LVNNSVLHLKNVXIQEFLDXVVKCFFILRASFRFCLKDIPNGL-GQF 176
```

RESULT 12
US-09-724-653-2
```
; Sequence 2, Application US/0972465
; Patent No. 6830913
; GENERAL INFORMATION:
; APPLICANT: Ling, Victor
; TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: AP2-004CP
; CURRENT APPLICATION NUMBER: US/09/724,653
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/167,930
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 2
; LENGTH: 766
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-653-2

Query Match            6.6%;   Score 78.5;   DB 2;   Length 766;
Best Local Similarity  18.0%;  Pred. No. 6.7;
Matches  34;   Conservative  39;   Mismatches  59;  Indels  57;  Gaps  8;

Qy   58 FVTFDLLFVTLLWIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRKVLI----- 112
            |:|:|       |:::|||:::              :| :|:||  :
Db   13 FMSVDICVTTAIYVF-----SHLDRSLLEDIRHFNIFDSVLDLWAACLYRSCLLLGATIG 67

Qy  113 ----LAYAVCRLR-HWWAIALTTAVTSAFLLAKVILSKLFSQ-------GAFGY 154
            |||   |:|:      ||:|:::      :::|  :|::|||          |
Db   68 VAKNSALGPRRLRASWLVITLVCLFVGIYAMVKLL---LFSEVRRPIRDPWFWALFVWTY 124

Qy  155 VLPISFILAWIETWFLDFKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFY----- 209
            ||||  :|:|    ||:   |:      :: :|||   | |   |:|  :|
Db  125 ISLGASFLLWL------------------------LSTVRPGTQ--ALEPGAATEAEGFPGSGR 163

Qy  210 SPPESEAGS 218
            ||| |:|:
Db  164 PPPEQASGA 172
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RESULT 13
US-09-724-653-14
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; Sequence 14, Application US/0972465
; Patent No. 6830913
; GENERAL INFORMATION:
; APPLICANT: Ling, Victor
; TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: AP2-004CP
; CURRENT APPLICATION NUMBER: US/09/724,653
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/167,930
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 14
; LENGTH: 766
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-653-14

Query Match            6.6%;   Score 78.5;   DB 2;   Length 766;
Best Local Similarity  18.0%;  Pred. No. 6.7;
Matches  34;   Conservative  39;   Mismatches  59;  Indels  57;  Gaps  8;

Qy   58 FVTFDLLFVTLLWIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRKVLI----- 112
            |:|:|       |:::|||:::              :| :|:||  :
Db   13 FMSVDICVTTAIYVF-----SHLDRSLLEDIRHFNIFDSVLDLWAACLYRSCLLLGATIG 67

Qy  113 ----LAYAVCRLR-HWWAIALTTAVTSAFLLAKVILSKLFSQ-------GAFGY 154
            |||   |:|:      ||:|:::      :::|  :|::|||          |
Db   68 VAKNSALGPRRLRASWLVITLVCLFVGIYAMVKLL---LFSEVRRPIRDPWFWALFVWTY 124

Qy  155 VLPISFILAWIETWFLDFKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFY----- 209
            ||||  :|:|    ||:   |:      :: :|||   | |   |:|  :|
Db  125 ISLGASFLLWL------------------------LSTVRPGTQ--ALEPGAATEAEGFPGSGR 163

Qy  210 SPPESEAGS 218
            ||| |:|:
Db  164 PPPEQASGA 172
```

RESULT 14
US-09-724-653-15
```
; Sequence 15, Application US/0972465
; Patent No. 6830913
; GENERAL INFORMATION:
; APPLICANT: Ling, Victor
; TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: AP2-004CP
; CURRENT APPLICATION NUMBER: US/09/724,653
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/167,930
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 15
; LENGTH: 766
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-653-15

Query Match            6.6%;   Score 78.5;   DB 2;   Length 766;
Best Local Similarity  18.0%;  Pred. No. 6.7;
Matches  34;   Conservative  39;   Mismatches  59;  Indels  57;  Gaps  8;

Qy   58 FVTFDLLFVTLLWIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRKVLI----- 112
            |:|:|       |:::|||:::              :| :|:||  :
Db   13 FMSVDICVTTAIYVF-----SHLDRSLLEDIRHFNIFDSVLDLWAACLYRSCLLLGATIG 67

Qy  113 ----LAYAVCRLR-HWWAIALTTAVTSAFLLAKVILSKLFSQ-------GAFGY 154
            |||   |:|:      ||:|:::      :::|  :|::|||          |
Db   68 VAKNSALGPRRLRASWLVITLVCLFVGIYAMVKLL---LFSEVRRPIRDPWFWALFVWTY 124

Qy  155 VLPISFILAWIETWFLDFKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFY----- 209
            ||||  :|:|    ||:   |:      :: :|||   | |   |:|  :|
Db  125 ISLGASFLLWL------------------------LSTVRPGTQ--ALEPGAATEAEGFPGSGR 163

Qy  210 SPPESEAGS 218
            ||| |:|:
Db  164 PPPEQASGA 172
```

RESULT 15
US-09-248-796A-20444
Sequence 20444, Application US/0924879GA
Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20444
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20444

Query Match   6.5%;   Score 78; DB 2; Length 228;
Best Local Similarity 22.1%;   Pred. No 1.4;
Matches   32; Conservative 32; Mismatches 49; Indels 32; Gaps   7;

Qy   63 LLFVTL-----LWIIELNVN---GGIENTLEKEVMQQYDYYSSYF--------DIFLLAVE 106
          :||:| ||:| :|:| :|:|| |
Db   91 LVFFALTSYGAFWLSFAAINIPTFGILAAYQKDMTQLSSALAFYLIIAWAILSFIFMLLTF 150

Qy   107 RFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISF----- 161
          : ||:| |:| ::|::::: ||| : ||| : : :
Db   151 KSTVLLSGFFLC------LTALFSLLSASYFVGGSVALTK--AAGAFGVIAVVAALYDTFA 202

Qy   162 ILAWIETWFLDFKVLP----QEAEEE 183
          ::|:| |:|| |:|:|
Db   203 LLATKQNSYFTLPVIPLPGGSEAKQE 227

Search completed: October 31, 2006, 02:25:23
Job time : 74 secs

OM protein - protein search, using sw model

GenCore version 5.1.9
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Run on: October 31, 2006, 02:32:24 ; Search time 185 seconds
      (without alignments)
      585.904 Million cell updates/sec

Sequence: 1 MNHLPEDMENALTGSQSSHA.........EAGSEAEAEKQDSEKPLLEL 234

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      Gapop 10.0 , Gapext 0.5

Perfect score: 1195

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
      Maximum Match 100%
      Listing first 1500 summaries

Database :
  Published Applications AA Main:*
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  2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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  5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
  6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
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466	1195	100.0	234	4	US-10-223-084-62	Sequence 62, Appl
467	1195	100.0	234	4	US-10-223-088-62	Sequence 62, Appl
468	1195	100.0	234	4	US-10-223-090-62	Sequence 62, Appl
470	1195	100.0	234	4	US-10-223-087-62	Sequence 62, Appl
478	1195	100.0	234	4	US-10-223-083-62	Sequence 62, Appl
481	1195	100.0	234	4	US-10-223-089-62	Sequence 62, Appl
498	1195	100.0	234	4	US-10-174-587-66	Sequence 66, Appl
562	1195	100.0	234	4	US-10-063-742-14	Sequence 14, Appl
640	1195	100.0	234	4	US-10-223-081-62	Sequence 62, Appl
650	1195	100.0	234	4	US-10-223-082-62	Sequence 62, Appl
665	1195	100.0	234	4	US-10-144-194A-20	Sequence 20, Appl
670	1195	100.0	234	4	US-10-305-654-62	Sequence 62, Appl
675	1195	100.0	234	4	US-10-491-056-62	Sequence 62, Appl
681	1195	100.0	234	4	US-10-081-056-62	Sequence 62, Appl
682	1195	100.0	234	5	US-10-972-317-14	Sequence 14, Appl
683	1195	100.0	234	5	US-10-485-555-36	Sequence 36, Appl
692	1195	100.0	234	6	US-11-102-240-14	Sequence 14, Appl
693	1195	100.0	234	6	US-11-103-195-14	Sequence 14, Appl
694	1188	99.4	234	4	US-10-262-839-84	Sequence 84, Appl
695	1024	85.7	201	4	US-10-264-237-2663	Sequence 2663, Ap
696	985	82.4	198	4	US-10-262-839-82	Sequence 82, Appl
697	669.5	56.0	176	6	US-11-072-512-2567	Sequence 2567, Ap
698	669.5	56.0	176	6	US-10-104-047-2567	Sequence 2567, Ap
699	664	55.6	445	4	US-11-177-293-296	Sequence 296, App
700	664	55.6	445	4	US-10-435-696-33	Sequence 33, Appl
701	625	52.3	534	5	US-10-450-763-35857	Sequence 35857, A
702	578	48.4	412	5	US-10-491-213-22	Sequence 22, Appl
703	343	28.7	580	6	US-11-097-143-6696	Sequence 6696, Ap
704	91	7.6	373	4	US-10-091-007-198	Sequence 198, App
705	90.5	7.6	803	4	US-10-437-963-136814	Sequence 136814,
706	87.5	7.3	516	3	US-09-925-298-653	Sequence 653, App
707	87.5	7.3	516	4	US-10-102-806-653	Sequence 653, App
708	87	7.3	421	5	US-10-741-600-929	Sequence 929, App
709	85.5	7.2	223	5	US-10-741-600-926	Sequence 926, App
710	85.5	7.2	285	5	US-10-741-600-928	Sequence 928, App
711	85.5	7.2	315	5	US-10-741-600-925	Sequence 925, App
712	85.5	7.2	323	4	US-10-741-600-923	Sequence 923, App
713	85.5	7.2	338	5	US-10-741-600-924	Sequence 924, App
714	85.5	7.2	339	5	US-10-741-600-930	Sequence 930, App
715	85.5	7.2	384	5	US-10-741-600-927	Sequence 927, App
716	85.5	7.2	390	4	US-10-741-600-928	Sequence 928, App
717	85.5	7.2	396	4	US-10-741-600-932	Sequence 932, App
718	85.5	7.2	396	4	US-10-282-122A-54604	Sequence 54604, A
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720	85.5	7.2	438	5	US-10-262-511-182	Sequence 182, App
721	85.5	7.2	440	4	US-10-262-511-182	Sequence 182, App
722	85.5	7.2	384	5	US-10-237-2016	Sequence 2016, App
723	85.5	7.2	473	4	US-10-821-234-1075	Sequence 1075, App
724	85.5	7.2	473	4	US-10-723-860-872	Sequence 872, App
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726	85	7.1	500	4	US-10-282-122A-334089	Sequence 334089,
727	85	7.1	527	4	US-10-425-114-65247	Sequence 65247, A
728	85	7.1	797	5	US-10-156-761-11433	Sequence 11433, A
729	85	7.1	797	4	US-10-732-923-22362	Sequence 22362, A
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731	84.5	7.1	886	4	US-10-282-122A-61134	Sequence 61134, A
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734	82.5	6.9	341	4	US-10-282-122A-63532	Sequence 63532, A
735	82.5	6.9	341	4	US-10-216-209-92	Sequence 92, Appl
736	82.5	6.9	389	5	US-10-831-070-126	Sequence 126, App
737	82.5	6.9	389	5	US-10-205-194-144	Sequence 144, App
738	82	6.9	1466	5	US-10-732-923-1543	Sequence 1543, App
739	81.5	6.8	264	4	US-11-096-568A-29540	Sequence 29540, A
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742	81	6.8	525	4	US-10-425-115-253855	Sequence 253855,
743	81	6.8	529	4	US-10-369-493-5808	Sequence 5808, App
744	81	6.8	529	4	US-10-369-493-5809	Sequence 5809, App
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755	80	6.7	360	3	US-11-264-096-1308	Sequence 1308, App
756	80	6.7	516	4	US-10-425-114-37103	Sequence 37103, A
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760	79.5	6.7	406	4	US-11-087-099-5751	Sequence 5751, Ap
761	79.5	6.7	463	4	US-10-425-115-314242	Sequence 314242,
762	79.5	6.7	558	4	US-11-097-143-2241	Sequence 2241, Ap
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764	79.5	6.7	723	4	US-10-335-977-8880	Sequence 8880, App
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770	79	6.6	777	4	US-10-353-690-110	Sequence 110, App
771	79	6.6	1531	4	US-09-832-202-35	Sequence 35, Appl
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774	78.5	6.6	228	5	US-10-501-282-4244	Sequence 4244, Ap
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779	78.5	6.6	754	5	US-10-330-773-72	Sequence 72, Appl
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791	78	6.5	355	4	US-10-661-798-9	Sequence 9, Appli
792	78	6.5	355	4	US-10-612-791-9	Sequence 9, Appli
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797	77.5	6.5	280	4	US-10-450-763-47733	Sequence 47733, A
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813	76.5	6.4	195	6	US-11-096-568A-2316	Sequence 2316, Ap
814	76.5	6.4	215	6	US-11-096-568A-2313	Sequence 2313, Ap
815	76.5	6.4	224	6	US-11-096-568A-4310	Sequence 4310, Ap
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833	76	6.4	1402	4	US-10-362-493-5502	Sequence 5502, Ap
834	76	6.4	1551	6	US-10-732-923-1738	Sequence 1738, Ap
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841	75.5	6.3	263	3	US-10-873-528-119	Sequence 119, App
842	75.5	6.3	264	5	US-10-611-320-4877	Sequence 4877, Ap
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845	75.5	6.3	342	4	US-10-451-467A-528	Sequence 528, App
846	75.5	6.3	342	5	US-09-911-020-293	Sequence 293, App
847	75.5	6.3	352	5	US-10-771-241-293	Sequence 293, App
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857	75	6.3	473	4	US-10-755-889-598	Sequence 598, App
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872	74.5	6.2	355	4	US-10-251-385-232	Sequence 232, App
873	74.5	6.2	355	4	US-10-567A-249	Sequence 249, App
874	74.5	6.2	355	4	US-10-239-423-82	Sequence 82, Appl
875	74.5	6.2	355	4	US-10-741-601-367	Sequence 367, App
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877	74.5	6.2	355	6	US-10-723-860-958	Sequence 958, App
878	74.5	6.2	355	4	US-10-741-600-1084	Sequence 1084, Ap
879	74.5	6.2	355	4	US-10-995-561-636	Sequence 636, App
880	74.5	6.2	362	4	US-10-486-471-18	Sequence 18, Appl
881	74.5	6.2	362	4	US-10-741-601-368	Sequence 368, App
882	74.5	6.2	362	5	US-10-741-600-1085	Sequence 1085, Ap
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894	74	6.2	324	5	US-10-472-928-4900	Sequence 4900, Ap
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897	74	6.2	350	4	US-10-112-356-7	Sequence 7, Appli
898	74	6.2	350	4	US-10-222-567A-164	Sequence 164, App
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915	73.5	6.2	404	4	US-10-437-963-153088	Sequence 153088,
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917	73.5	6.2	491	4	US-10-738-986-31	Sequence 31, Appl
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919	73.5	6.2	573	4	US-11-079-463-9814	Sequence 9814, Ap
920	73.5	6.2	574	4	US-11-032-585-7411	Sequence 7411, Ap
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931	73	6.1	114	4	US-10-335-977-8879	Sequence 8879, Ap
932	73	6.1	189	3	US-10-828-644-114	Sequence 114, App
933	73	6.1	265	4	US-10-335-977-5926	Sequence 5926, Ap
934	73	6.1	272	4	US-10-912-456-75	Sequence 75, Appl
935	73	6.1	272	4	US-10-156-911-75	Sequence 75, Appl
936	73	6.1	276	4	US-10-177-293-5928	Sequence 5928, Ap
937	73	6.1	322	4	US-10-335-977-5928	Sequence 5928, Ap
938	73	6.1	364	4	US-10-303-204-16	Sequence 16, Appl
939	73	6.1	377	3	US-09-939-980-533	Sequence 533, App
940	73	6.1	450	4	US-10-626-832-59	Sequence 59, Appl
941	73	6.1	453	4	US-10-282-122A-59343	Sequence 59343, A
942	73	6.1	469	5	US-10-213-974-40	Sequence 40, Appl
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944	73	6.1	526	5	US-09-746-783-806	Sequence 806, App
945	73	6.1	526	4	US-10-038-854-30	Sequence 30, Appl
946	73	6.1	553	4	US-10-455-772-782	Sequence 782, App
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949	73	6.1	748	3	US-11-097-143-40725	Sequence 40725, A
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952	73	6.1	750	4	US-10-689-742-86	Sequence 86, Appl
953	73	6.1	788	3	US-09-815-242-70316	Sequence 70316, A
954	73	6.1	792	4	US-10-282-122A-12327	Sequence 12327, A
955	73	6.1	792	4	US-10-470-048B-334	Sequence 334, App
956	73	6.1	806	4	US-10-437-963-173527	Sequence 173527,
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959	73	6.1	966	3	US-09-828-466-11	Sequence 11, Appli
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962	73	6.1	971	4	US-10-631-467-1411	Sequence 1411, Ap
963	73	6.1	971	4	US-10-624-727-49	Sequence 49, Appl
964	73	6.1	971	4	US-10-624-727-59	Sequence 59, Appl
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972	72.5	6.1	209	4	US-10-080-170-107	Sequence 107, App
973	72.5	6.1	209	4	US-10-080-170-107	Sequence 107, App
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1231	70.5	5.9	496	4	US-11-188-298-1008	Sequence 1008, Ap
1232	70.5	5.9	499	4	US-11-087-099-948	Sequence 948, App
1233	70.5	5.9	521	4	US-10-724-972A-5387	Sequence 5387, Ap
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1236	70.5	5.9	539	6	US-10-051-909-26	Sequence 26, Appl
1237	70.5	5.9	548	4	US-11-210-316-26	Sequence 26, Appl
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1241	70.5	5.9	740	4	US-10-051-909-37	Sequence 37, Appl
1242	70.5	5.9	740	4	US-10-437-963-195955	Sequence 195955,
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1244	70.5	5.9	1026	4	US-10-032-585-7591	Sequence 7591, Ap
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1247	70.5	5.9	1781	3	US-09-738-877-3	Sequence 3, Appli
1248	70.5	5.9	1781	6	US-10-428-487-16	Sequence 16, Appl
1249	70.5	5.9	1781	4	US-10-097-143-36162	Sequence 36162, A
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1251	70.5	5.9	1787	6	US-10-282-122A-63601	Sequence 63601, A
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1255	70.5	5.9	256	5	US-11-097-143-30	Sequence 30, Appl
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1260	70.5	5.9	311	4	US-09-908-006A-41	Sequence 41, Appl
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1262	70.5	5.9	333	4	US-11-251-385-172	Sequence 172, App
1263	70.5	5.9	333	4	US-10-225-567A-279	Sequence 279, App
1264	70.5	5.9	333	4	US-10-433-561-32	Sequence 32, Appl
1265	70.5	5.9	333	4	US-10-477-726-4	Sequence 4, Appli
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1268	70.5	5.9	333	5	US-11-788-197-75	Sequence 75, Appl
1269	70.5	5.9	333	4	US-10-500-175A-4	Sequence 4, Appli
1270	70.5	5.9	333	6	US-10-311-019B-4	Sequence 4, Appli
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1276	70.5	5.9	364	5	US-10-788-197-79	Sequence 79, Appl
1277	70.5	5.9	364	5	US-10-901-772-56	Sequence 56, Appl
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1284	70.5	5.9	399	4	US-10-989-861-17	Sequence 17, Appl
1285	70.5	5.9	471	3	US-09-989-749-1978	Sequence 1978, Ap
1286	70	5.9	475	4	US-10-297-022-24	Sequence 24, Appl

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1292	70	5.9	532	4	US-11-087-099-8860	Sequence 8860, Ap
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1298	70	5.9	640	3	US-11-123-241-123	Sequence 123, App
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1311	69.5	5.8	247	4	US-10-501-282-3218	Sequence 3218, Ap
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1313	69.5	5.8	257	4	US-10-767-701-45706	Sequence 45706, A
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1316	69.5	5.8	296	4	US-10-746-795-24	Sequence 24, Appl
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1320	69.5	5.8	308	4	US-09-804-291-453	Sequence 453, App
1321	69.5	5.8	308	4	US-09-981-566-51	Sequence 51, Appl
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1324	69.5	5.8	308	4	US-10-292-798-786	Sequence 786, App
1325	69.5	5.8	317	4	US-10-343-650A-216	Sequence 216, App
1326	69.5	5.8	318	4	US-11-096-568A-6964	Sequence 6964, Ap
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1337	69.5	5.8	415	6	US-11-045-004-318	Sequence 318, App
1338	69.5	5.8	421	5	US-10-097-143-9636	Sequence 9636, Ap
1339	69.5	5.8	428	4	US-11-096-568A-20717	Sequence 20717, A
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1342	69.5	5.8	461	4	US-10-369-493-5002	Sequence 5002, Ap
1343	69.5	5.8	477	4	US-10-732-923-4293	Sequence 4293, Ap
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1346	69.5	5.8	491	6	US-10-425-115-293577	Sequence 293577,
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1351	69.5	5.8	557	4	US-10-762-154-1	Sequence 1, Appli
1352	69.5	5.8	557	4	US-10-327-188-4	Sequence 4, Appli
1353	69.5	5.8	557	4	US-10-450-500-1	Sequence 1, Appli
1354	69.5	5.8	568	4	US-10-264-237-33388	Sequence 33388, A
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1357	69.5	5.8	573	4	US-11-072-512-3669	Sequence 3669, Ap
1358	69.5	5.8	579	4	US-10-282-122A-60627	Sequence 60627, A
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1360	69.5	5.8	584	6	US-11-188-298-21635	Sequence 21635, A
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1368	69.5	5.8	801	4	US-10-282-122A-71745	Sequence 71745, A
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1373	69.5	5.8	1010	4	US-10-282-122A-44559	Sequence 44559, A
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1375	69.5	5.8	154	5	US-10-501-282-3214	Sequence 3214, Ap
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1377	69.5	5.8	214	4	US-10-408-765A-2220	Sequence 2220, Ap
1378	69.5	5.8	214	4	US-10-648-593-213	Sequence 213, App
1379	69.5	5.8	214	4	US-10-072-175-213	Sequence 213, A
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1385	69.5	5.8	321	6	US-11-108-260A-2534	Sequence 2534, Ap
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1387	69.5	5.8	368	4	US-10-965-103-9	Sequence 9, Appli
1388	69.5	5.8	370	3	US-11-054-211-104	Sequence 104, Appl
1389	69.5	5.8	370	6	US-11-116-727-46	Sequence 46, Appl
1390	69.5	5.8	370	4	US-10-611-210-11	Sequence 11, Appl
1391	69.5	5.8	370	4	US-09-741-669-370	Sequence 370, Appl
1392	69.5	5.8	370	3	US-10-912-020-378	Sequence 378, App
1393	69.5	5.8	370	6	US-11-188-298-6833	Sequence 6833, Ap
1394	69.5	5.8	370	3	US-10-424-599-184014	Sequence 184014,
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1397	69.5	5.8	370	4	US-10-044-592-12	Sequence 12, Appl
1398	69.5	5.8	370	4	US-10-044-592-74	Sequence 74, Appl
1399	69.5	5.8	370	4	US-10-225-567A-245	Sequence 245, Appl
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1403	69.5	5.8	370	6	US-11-116-727-46	Sequence 46, Appl
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1429	69	5.8	2310	3	US-09-995-542-10	Sequence 10, Appli
1430	69	5.8	5127	5	US-10-668-767-8	Sequence 8, Appli
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1440	68.5	5.7	200	4	US-11-167-831-36	Sequence 36, Appl
1441	68.5	5.7	209	4	US-10-001-887-86	Sequence 86, Appl
1442	68.5	5.7	209	6	US-10-958-863-86	Sequence 86, Appl
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1446	68.5	5.7	227	4	US-10-504-582-140	Sequence 140, App
1447	68.5	5.7	282	4	US-10-424-599-160679	Sequence 160679,
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1458	68.5	5.7	377	3	US-10-732-923-4899	Sequence 4899, Ap
1459	68.5	5.7	377	4	US-10-115-571A-9	Sequence 9, Appli
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1463	68.5	5.7	382	4	US-10-087-192-783	Sequence 783, App
1464	68.5	5.7	383	5	US-10-100-593-8	Sequence 8, Appli
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1470	68.5	5.7	444	3	US-09-853-386-136	Sequence 136, App
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1472	68.5	5.7	444	4	US-10-242-822B-2	Sequence 2, Appli
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1475	68.5	5.7	468	3	US-11-292-709-708	Sequence 708, App
1476	68.5	5.7	468	5	US-09-826-509-553	Sequence 553, App
1477	68.5	5.7	468	3	US-11-292-990-638	Sequence 638, App
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217	69	5.8	326	7	US-11-056-355B-71810	Sequence 71810, A
218	69	5.8	326	7	US-11-471-571A-4042	Sequence 4042, A
219	69	5.8	350	7	US-10-449-902-50010	Sequence 50010, A
220	69	5.8	355	7	US-10-953-349-22057	Sequence 22057, A
221	69	5.8	440	6	US-11-056-355B-58390	Sequence 58390, A
222	69	5.8	440	7	US-11-056-355B-58389	Sequence 58389, A
223	69	5.8	450	7	US-11-056-355B-450	Sequence 450, App
224	69	5.8	450	7	US-10-953-349-5613	Sequence 5613, Ap
225	69	5.8	508	7	US-10-953-349-5612	Sequence 5612, Ap
226	69	5.8	520	7	US-11-056-355B-36301	Sequence 36301, A
227	69	5.8	520	7	US-11-056-355B-36302	Sequence 36302, A
228	69	5.8	520	6	US-10-449-902-50472	Sequence 50472, A
229	69	5.8	526	6	US-10-449-902-50106	Sequence 50106, A
230	69	5.8	526	6	US-10-449-902-48588	Sequence 48588, A
231	69	5.8	526	7	US-11-056-355B-36835	Sequence 36835, A
232	69	5.8	526	7	US-11-264-544A-14	Sequence 95, Appl
233	69	5.8	526	7	US-11-264-784-82	Sequence 123, App
234	69	5.8	526	7	US-11-265-761-95	Sequence 82, Appl
235	69	5.8	526	7	US-11-190-750-84	Sequence 84, Appl
236	69	5.8	526	7	US-11-190-750-80	Sequence 80, Appl
237	69	5.8	569	6	US-11-024-544A-14	Sequence 12, Appl
238	69	5.8	569	6	US-11-024-544A-12	Sequence 14, Appl
239	69	5.8	569	6	US-11-199-489A-94	Sequence 8817, Ap
240	69	5.8	569	6	US-11-330-403-5831	Sequence 5831, Ap
241	69	5.8	647	6	US-10-449-902-50472	Sequence 94, Appl
242	69	5.8	211	7	US-11-056-355B-72029	Sequence 72029, A
243	68.5	5.7	218	7	US-11-056-355B-91424	Sequence 91424, A
244	68.5	5.7	220	7	US-11-056-355B-95180	Sequence 95180, A
245	68.5	5.7	220	7	US-11-333-747A-144	Sequence 144, App
246	68.5	5.7	227	7	US-11-333-747A-144	Sequence 144, App

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248	68.5	5.7	233	7	US-11-056-355B-91423	Sequence 91423, A
249	68.5	5.7	233	7	US-11-056-355B-95179	Sequence 95179, A
250	68.5	5.7	287	6	US-11-305-666-85	Sequence 85, Appl
251	68.5	5.7	378	6	US-10-669-920-490	Sequence 490, App
252	68.5	5.7	435	7	US-11-056-355B-91465	Sequence 91465, A
253	68.5	5.7	435	7	US-11-056-355B-95221	Sequence 95221, A
254	68.5	5.7	444	7	US-11-358-841-2	Sequence 2, Appli
255	68.5	5.7	468	7	US-11-404-939-553	Sequence 553, App
256	68.5	5.7	500	7	US-11-056-355B-91464	Sequence 91464, A
257	68.5	5.7	500	7	US-11-056-355B-95220	Sequence 95220, A
258	68.5	6	501	7	US-10-449-902-46991	Sequence 46991, A
259	68.5	5.7	501	7	US-11-056-355B-91477	Sequence 91477, A
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262	68.5	5.7	528	7	US-11-056-355B-79432	Sequence 79432, A
263	68.5	5.7	590	7	US-11-056-355B-79430	Sequence 79430, A
264	68.5	5.7	643	7	US-11-056-355B-91476	Sequence 91476, A
265	68.5	5.7	643	7	US-11-056-355B-95232	Sequence 95232, A
266	68.5	5.7	653	7	US-11-056-355B-91475	Sequence 91475, A
267	68.5	5.7	653	7	US-11-056-355B-95231	Sequence 95231, A
268	68.5	5.7	894	7	US-11-056-355B-5482	Sequence 5482, Ap
269	68.5	5.7	894	7	US-11-434-137-5482	Sequence 5482, Ap
270	68.5	5.7	894	7	US-11-434-184-8898	Sequence 8898, Ap
271	68.5	5.7	894	7	US-11-434-199-8898	Sequence 8898, Ap
272	68.5	5.7	894	6	US-11-293-697-4304	Sequence 4304, Ap
273	68.5	5.7	894	7	US-11-434-199-5482	Sequence 5482, Ap
274	68.5	5.7	894	7	US-11-434-203-5482	Sequence 5482, Ap
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276	68.5	5.7	247	6	US-10-805-394-5109	Sequence 5109, Ap
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278	68.5	5.7	312	6	US-10-449-902-43616	Sequence 43616, A
279	68.5	5.7	330	7	US-11-434-199-5614	Sequence 5614, Ap
280	68.5	5.7	330	7	US-11-056-355B-23626	Sequence 23626, A
281	68.5	5.7	330	7	US-11-056-355B-36303	Sequence 36303, A
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283	68.5	5.7	342	6	US-11-403-051-55	Sequence 55, Appl
284	68.5	5.7	344	7	US-11-434-203-396	Sequence 396, App
285	68.5	5.7	344	6	US-11-434-199-396	Sequence 396, App
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293	68.5	5.7	388	6	US-10-487A-769	Sequence 769, App
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295	68.5	5.7	488	7	US-11-404-939-561	Sequence 561, App
296	68.5	5.7	689	6	US-10-449-902-45629	Sequence 45629, A
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301	68	5.7	2359	6	US-10-543-503-134	Sequence 134, App
302	68	5.7	3010	7	US-11-056-355B-50506	Sequence 50506, A
303	68	5.7	3010	7	US-11-140-487A-769	Sequence 769, App
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305	67.5	5.6	250	6	US-11-056-355B-49321	Sequence 49321, A
306	67.5	5.6	286	7	US-11-056-355B-51767	Sequence 51767, A
307	67.5	5.6	286	6	US-10-305-666-64	Sequence 64, Appl
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309	67.5	5.6	321	7	US-11-056-355B-11207	Sequence 11207, A
310	67.5	5.6	348	6	US-11-056-355B-11206	Sequence 11206, A
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314	67.5	5.6	431	7	US-11-434-137-3244	Sequence 3244, Ap
315	67.5	5.6	431	7	US-11-434-184-3244	Sequence 3244, Ap
316	67.5	5.6	431	7	US-11-434-199-3244	Sequence 3244, Ap
317	67.5	5.6	431	7	US-11-434-203-3244	Sequence 3244, Ap
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324	67.5	5.6	933	7	US-11-248-130-138	Sequence 138, App
325	67	5.6	158	7	US-11-434-137-2484	Sequence 2484, Ap
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328	67	5.6	158	7	US-11-434-203-2484	Sequence 2484, Ap
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330	67	5.6	179	7	US-11-056-355B-40233	Sequence 40233, A
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335	67	5.6	287	7	US-11-434-199-3540	Sequence 3540, Ap
336	67	5.6	287	7	US-11-434-203-3540	Sequence 3540, Ap
337	67	5.6	290	6	US-10-449-902-31146	Sequence 31146, A
338	67	5.6	295	7	US-11-056-355B-50168	Sequence 50168, A
339	67	5.6	320	7	US-11-056-355B-50169	Sequence 50169, A
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341	67	5.6	320	7	US-11-056-355B-56253	Sequence 56253, A
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351	67	5.6	743	7	US-11-434-199-3596	Sequence 3596, Ap
352	67	5.6	746	7	US-11-056-355B-87569	Sequence 87569, A
353	67	5.6	756	7	US-11-056-355B-69594	Sequence 69594, A
354	67	5.6	804	6	US-11-056-355B-50168	Sequence 50168, A
355	67	5.6	814	7	US-11-056-355B-87568	Sequence 87568, A
356	67	5.6	1804	7	US-11-056-355B-75729	Sequence 75729, A
357	67	5.6	1809	7	US-11-056-355B-87721	Sequence 87721, A
358	67	5.6	1811	6	US-11-056-355B-75728	Sequence 75728, A
359	67	5.6	1816	7	US-11-056-355B-87720	Sequence 87720, A
360	67	5.6	1816	7	US-11-056-355B-75727	Sequence 75727, A
361	67	5.6	1856	7	US-11-056-355B-87719	Sequence 87719, A
362	67	5.6	3502	6	US-11-063-439-160	Sequence 160, App
363	66.5	5.6	415	7	US-11-056-355B-28244	Sequence 28244, A
364	66.5	5.6	403	7	US-11-056-355B-31834	Sequence 31834, A
365	66.5	5.6	359	6	US-11-056-355B-77217	Sequence 77217, A
366	66.5	5.6	371	6	US-10-471-571A-34722	Sequence 34722, A
367	66.5	5.6	384	6	US-11-056-355B-77217	Sequence 77217, A
368	66.5	5.6	384	6	US-10-511-928-263	Sequence 263, App
369	66.5	5.6	392	7	US-10-953-349-34721	Sequence 34721, A
370	66.5	5.6	384	7	US-11-056-355B-34721	Sequence 34721, A
371	66.5	5.6	392	7	US-11-056-355B-72708	Sequence 72708, A
372	66.5	5.6	403	7	US-10-471-571A-4720	Sequence 4720, Ap
373	66.5	5.6	453	7	US-10-471-571A-2520	Sequence 2520, Ap
374	66.5	5.6	453	7	US-10-449-902-52191	Sequence 52191, A
375	66.5	5.6	455	7	US-11-330-403-3789	Sequence 3789, Ap
376	66.5	5.6	455	7	US-10-471-571A-4822	Sequence 4822, Ap
377	66.5	5.6	457	6	US-11-056-355B-51106	Sequence 51106, A
378	66.5	5.6	459	7	US-11-612-783-4310	Sequence 4310, Ap
379	66.5	5.6	499	7	US-11-434-203-3562	Sequence 3562, Ap
380	66.5	5.6	499	7	US-11-434-137-3562	Sequence 3562, Ap
381	66.5	5.6	499	7	US-11-434-184-3562	Sequence 3562, Ap
382	66.5	5.6	499	7	US-11-434-199-3562	Sequence 3562, Ap
383	66.5	5.6	504	6	US-11-570-509-4	Sequence 4, Appli
384	66.5	5.6	551	7	US-11-540-898-67	Sequence 67, Appl
385	66.5	5.6	772	6	US-10-540-898-67	Sequence 67, Appl
386	66.5	5.6	830	7	US-11-449-902-41424	Sequence 41424, A
387	66.5	5.6	881	6	US-10-511-937-2474	Sequence 2474, Ap
388	66.5	5.6	1383	7	US-10-449-902-41424	Sequence 41424, A
389	66.5	5.6	1530	6	US-11-301-094-2	Sequence 2, Appli
390	66	5.6	151	7	US-10-534-774-24	Sequence 24, Appl
391	66	5.6	3010	6	US-10-449-902-41309	Sequence 41309, A
392	66	5.5	217	6	US-11-366-965-1129	Sequence 1129, Ap
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395	66	5.5	238	6	US-11-056-355B-105779	Sequence 105779,
396	66	5.5	238	7	US-11-056-355B-117018	Sequence 117018,
397	66	5.5	253	6	US-10-953-349-28669	Sequence 28669, A
398	66	5.5	288	7	US-10-953-349-6922	Sequence 6922, App
399	66	5.5	354	6	US-10-516-032-10	Sequence 10, Appl
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401	66	5.5	389	7	US-11-434-137-5792	Sequence 5792, Ap
402	66	5.5	389	7	US-11-434-184-5792	Sequence 5792, Ap
403	66	5.5	389	7	US-11-434-199-5792	Sequence 5792, Ap
404	66	5.5	389	7	US-11-434-203-5792	Sequence 5792, Ap
405	66	5.5	405	7	US-11-412-025-38	Sequence 38, Appl
406	66	5.5	410	7	US-11-366-965-908	Sequence 908, App
407	66	5.5	412	6	US-11-366-571A-2744	Sequence 2744, Ap
408	66	5.5	447	7	US-10-538-198-2	Sequence 2, Appli
409	66	5.5	450	6	US-10-538-198-1	Sequence 4, Appli
410	66	5.5	461	6	US-10-805-394-5041	Sequence 5041, Ap
411	66	5.5	739	6	US-10-449-902-41118	Sequence 41118, A
412	66	5.5	807	6	US-10-449-902-40810	Sequence 40810, A
413	66	5.5	3498	7	US-11-063-439-209	Sequence 209, App
414	66	5.5	3499	7	US-11-063-439-222	Sequence 222, App
415	66	5.5	3507	7	US-11-063-439-215	Sequence 215, App
416	66	5.5	3511	7	US-11-063-439-201	Sequence 201, App
417	65.5	5.5	304	6	US-10-449-902-6200	Sequence 6200, Ap
418	65.5	5.5	314	6	US-10-449-902-51124	Sequence 51124, A
419	65.5	5.5	444	6	US-10-511-937-3003	Sequence 3003, Ap
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423	65.5	5.5	550	6	US-10-449-902-48640	Sequence 48640, A
424	65.5	5.5	740	7	US-10-449-902-230	Sequence 230, App
425	65.5	5.5	801	6	US-11-251-208-230	Sequence 230, App
426	65.5	5.5	860	6	US-10-530-187-282	Sequence 282, App
427	65.5	5.5	1143	6	US-10-471-571A-258	Sequence 258, App
428	65.5	5.5	1146	7	US-11-226-554-148	Sequence 148, App
429	65.5	5.5	1152	7	US-11-226-554-147	Sequence 147, App
430	65.5	5.5	1152	7	US-11-248-718-148	Sequence 148, App
431	65.5	5.5	1152	7	US-11-248-718-147	Sequence 147, App
432	65.5	5.5	179	7	US-11-434-137-6692	Sequence 6692, Ap
433	65.5	5.4	179	7	US-11-434-184-6692	Sequence 6692, Ap
434	65.5	5.4	179	7	US-11-434-199-6692	Sequence 6692, Ap
435	65.5	5.4	179	7	US-11-434-203-6692	Sequence 6692, Ap
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445	65.5	5.4	290	6	US-10-449-902-45137	Sequence 45137, A
446	65.5	5.4	305	7	US-11-305-666-69	Sequence 69, Appl
447	65.5	5.4	325	6	US-11-366-965-1067	Sequence 1067, Ap
448	65.5	5.4	325	6	US-10-953-349-6641	Sequence 6641, Ap
449	65.5	5.4	325	7	US-11-056-355B-23421	Sequence 23421, A
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452	65.5	5.4	370	6	US-11-358-841-7	Sequence 6, Appli
453	65.5	5.4	375	6	US-11-358-841-3	Sequence 3, Appli
454	65.5	5.4	375	6	US-11-412-025-6	Sequence 6, Appli
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457	65.5	5.4	415	7	US-11-358-841-1	Sequence 1, Appli
458	65.5	5.4	415	7	US-11-404-939-483	Sequence 483, App
459	65.5	5.4	415	7	US-11-412-025-2	Sequence 2, Appli
460	65.5	5.4	415	7	US-11-412-025-4	Sequence 4, Appli
461	65.5	5.4	415	7	US-11-412-025-40	Sequence 40, Appl
462	65.5	5.4	477	7	US-11-330-403-2009	Sequence 2009, Ap
463	65.5	5.4	490	7	US-11-330-403-1544	Sequence 1544, Ap
464	65.5	5.4	523	7	US-11-449-902-35714	Sequence 35714, A
465	65.5	5.4	530	6	US-10-471-571A-4590	Sequence 4590, Ap

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466	65	5.4	560	7	US-11-317-847A-144	Sequence 144, App
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469	65	5.4	661	7	US-11-056-355B-107830	Sequence 107830,
470	65	5.4	661	7	US-11-056-355B-119069	Sequence 119069,
471	65	5.4	673	7	US-11-056-355B-107829	Sequence 107829,
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647	63.5	5.3	685	7	US-11-090-997-710	Sequence 710, App
648	63.5	5.3	759	6	US-11-090-997-704	Sequence 704, App
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1241	60.5	5.1	3531	7	US-11-063-439-139	Sequence 139, App
1242	60.5	5.1	3534	7	US-11-063-439-132	Sequence 132, App
1243	60.5	5.1	3540	7	US-11-063-439-188	Sequence 188, App
1244	60.5	5.1	3541	7	US-11-063-439-128	Sequence 128, App
1245	60.5	5.1	3541	7	US-11-063-439-212	Sequence 212, App
1246	60.5	5.1	3542	7	US-11-063-439-158	Sequence 158, App
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1248	60.5	5.1	3544	7	US-11-063-439-197	Sequence 197, App
1249	60.5	5.1	3551	7	US-11-063-439-138	Sequence 138, App
1250	60.5	5.1	3551	7	US-11-063-439-120	Sequence 120, App
1251	60.5	5.1	3561	7	US-11-063-439-165	Sequence 165, App
1252	60.5	5.1	3568	7	US-11-063-439-150	Sequence 150, App
1253	60.5	5.1	3573	7	US-11-612-783-6739	Sequence 6739, Ap
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1255	60	5.1	167	7	US-11-056-355B-29728	Sequence 29728, A
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1258	60	5.1	205	7	US-10-449-902-32555	Sequence 32555, A
1259	60	5.1	205	7	US-10-449-902-42627	Sequence 42627, A
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1262	60	5.0	246	7	US-11-471-571A-1624	Sequence 1624, Ap
1263	60	5.0	246	7	US-11-056-355B-80675	Sequence 80675, A
1264	60	5.0	247	7	US-11-471-571A-1500	Sequence 1500, Ap
1265	60	5.0	258	6	US-10-449-902-43208	Sequence 43208, A
1266	60	5.0	258	6	US-11-056-355B-80675	Sequence 1624, Ap
1267	60	5.0	263	6	US-11-471-571A-1500	Sequence 1500, Ap
1268	60	5.0	266	6	US-10-449-902-32147	Sequence 32147, A
1269	60	5.0	266	6	US-10-449-902-32787	Sequence 32787, A
1270	60	5.0	266	6	US-10-449-902-54901	Sequence 54901, A

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1273	60	5.0	275	7	US-11-434-199-846	Sequence 846, App
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1275	60	5.0	279	6	US-10-449-902-35924	Sequence 35924, A
1276	60	5.0	309	6	US-10-953-349-17540	Sequence 17540, A
1277	60	5.0	309	7	US-11-056-355B-53298	Sequence 53298, A
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1279	60	5.0	309	6	US-11-073-360-191	Sequence 191, App
1280	60	5.0	310	6	US-10-953-349-6078	Sequence 6078, App
1281	60	5.0	310	7	US-11-056-355B-29541	Sequence 29541, A
1282	60	5.0	310	7	US-11-056-355B-33131	Sequence 33131, A
1283	60	5.0	322	6	US-11-404-939-509	Sequence 509, App
1284	60	5.0	333	7	US-11-471-571A-5328	Sequence 5328, Ap
1285	60	5.0	347	7	US-10-953-349-2272	Sequence 2272, App
1286	60	5.0	347	6	US-11-056-355B-40034	Sequence 40034, A
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1289	60	5.0	367	6	US-11-434-184-6806	Sequence 6806, Ap
1290	60	5.0	367	7	US-11-434-199-6806	Sequence 6806, Ap
1291	60	5.0	367	7	US-11-434-203-6806	Sequence 6806, Ap
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1293	60	5.0	395	7	US-11-330-403-1698	Sequence 1698, App
1294	60	5.0	400	7	US-11-056-355B-58959	Sequence 58959, A
1295	60	5.0	403	7	US-11-056-355B-47722	Sequence 47722, A
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1297	60	5.0	420	6	US-11-412-025-42	Sequence 42, Appl
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1303	60	5.0	463	6	US-11-434-199-900	Sequence 900, App
1304	60	5.0	463	7	US-11-434-203-900	Sequence 900, App
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1333	60	5.0	804	7	US-11-434-203-4630	Sequence 4630, Ap
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1338	60	5.0	908	7	US-11-073-360-157	Sequence 157, App
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1480	59	4.9	194	7	US-11-434-199-3424	Sequence 3424, Ap
1481	59	4.9	194	7	US-11-434-203-3424	Sequence 3424, Ap
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1495	59	4.9	294	6	US-10-476-107A-4	Sequence 4, Appli
1496	59	4.9	299	7	US-11-293-697-4207	Sequence 4207, Ap
1497	59	4.9	303	7	US-11-434-137-5234	Sequence 5234, Ap
1498	59	4.9	303	7	US-11-434-184-5234	Sequence 5234, Ap
1499	59	4.9	303	7	US-11-434-199-5234	Sequence 5234, Ap
1500	59	4.9	303	7	US-11-434-203-5234	Sequence 5234, Ap

Search completed: October 31, 2006, 02:38:38
Job time : 56 secs

QM protein - protein search, using sw model

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GenCore version 5.1.9

Run on: October 31, 2006, 02:24:29 ; Search time 43 Seconds
(without alignments)
523.598 Million cell updates/sec

Title: US-10-063-518-14
Perfect score: 1195
Sequence: 1 MNHLPEDMENALTGSQSSHA.........EAGSEEAEEKQDSEKPLLEL 234

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : 1: PIR_80:*
2: pir1:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	664	55.6	445	2	I38027	MLN 64 protein - h
2	204	17.1	478	2	T16170	hypothetical prote
3	102.5	8.6	348	2	H90281	hypothetical prote
4	93.5	7.8	424	2	D75080	glucose-1-phosphat
5	90	7.5	1911	2	T43048	calcium channel al
6	86.5	7.2	767	2	T21969	hypothetical prote
7	85.5	7.2	396	2	B81299	probable molybdopt
8	85	7.2	438	2	A57219	Batten disease-rel
9	85	7.1	448	2	G70172	conserved hypothet
10	84.5	7.1	471	2	A41680	integral membrane
11	83.5	7.0	352	2	H97002	probable integral
12	83	6.9	291	2	AE0302	sugar ABC transpor
13	83	6.9	590	1	S34960	NADH2 dehydrogenas
14	82.5	6.9	186	2	B29835	TraS protein - Esc
15	82.5	6.9	239	1	C64227	hypothetical prote
16	82.5	6.9	341	2	S51265	probable N-acetylg
17	82.5	6.9	406	2	T43120	conserved hypothet
18	82.5	6.9	891	2	T37397	major core protein
19	82	6.9	589	2	T52070	RNA1 protein homol
20	82	6.9	589	2	A36983	RNA1 homolog fug1
21	82	6.9	1466	2	T30566	ATP-binding casset
22	81	6.8	385	2	B84447	hypothetical prote
23	81	6.8	529	2	T23190	hypothetical prote
24	81	6.8	532	2	S46831	probable membrane
25	80.5	6.7	156	2	I84498	melatonin receptor
26	80.5	6.7	322	2	T45568	hypothetical prote
27	80.5	6.7	396	2	T50229	probable transmemb
28	80.5	6.7	417	2	C44038	tryptophan permeas
29	80.5	6.7	463	2	AE1155	amino acid transpo
30	80.5	6.7	536	2	A71491	probable integral
31	80.5	6.7	644	2	S63056	probable membrane
32	80.5	6.7	738	2	S106659	membrane protein t
33	80.5	6.7	891	1	WMVZ3S	major core protein
34	80.5	6.7	891	1	WMVZ3W	major core protein
35	80.5	6.7	1780	2	A85045	probable glucan sy
36	80	6.7	103	2	G75513	conserved hypothet
37	80	6.7	290	2	D89898	hypothetical prote
38	80	6.7	309	2	S59140	RTM1 protein - yea
39	80	6.7	388	1	H71115	hypothetical prote
40	80	6.7	1339	2	AF1532	probable SNF2 subf
41	79.5	6.7	463	2	AH1513	amino acid transpo
42	79.5	6.7	491	1	EDBEIC	immediate-early pr
43	78.5	6.6	239	2	S73812	spermidine/putresc
44	78.5	6.6	269	2	AF1532	hypothetical prote
45	78.5	6.6	358	2	F64136	rnfD protein homol
46	78.5	6.6	471	1	F64136	serotonin receptor
47	78.5	6.6	678	2	JC5346	IB3/5-polypeptide
48	78	6.6	245	2	S44925	cdd2 protein - Clo
49	78	6.6	259	2	F83825	hypothetical prote
50	78	6.6	382	2	E97157	stage III sporulat
51	78	6.5	471	2	F83825	hypothetical prote
52	78	6.5	2136	2	T39287	hypothetical prote
53	77.5	6.5	1297	2	A05037	spermidine/putresc
54	77.5	6.5	269	2	AH1175	hypothetical prote
55	77.5	6.5	299	2	AE0461	probable membrane
56	77.5	6.5	327	2	F82904	conserved hypothet
57	77.5	6.5	328	2	F84130	ABC transporter (p
58	77.5	6.5	338	2	T39159	hypothetical prote
59	77.5	6.5	440	2	T11319	NADH2 dehydrogenas
60	77.5	6.5	491	2	B69499	sodium- and chlori
61	77.5	6.5	512	2	AC3399	probable colanic b
62	77.5	6.5	734	1	DERZN5	NADH2 dehydrogenas
63	77.5	6.5	892	2	H72164	A11L protein - var
64	77.5	6.5	892	2	T28552	hypothetical prote
65	77.5	6.5	892	2	B36849	AlOI protein - var
66	77.5	6.5	1784	2	E81435	sodium channel pro
67	77	6.4	332	2	JC5919	probable secretion
68	77	6.4	362	2	AF0692	hypothetical trans
69	77	6.4	559	2	A71918	hypothetical prote
70	77	6.4	559	2	T41545	NADH2 dehydrogenas
71	77	6.4	590	2	T24184	hypothetical prote
72	77	6.4	650	1	T11476	multidrug resistan
73	77	6.4	991	2	T01377	hypothetical prote
74	77	6.4	1025	2	T18376	hypothetical prote
75	76.5	6.4	1117	2	C85018	phage tail fibe
76	76.5	6.4	1500	2	G84922	probable tail prot
77	76.5	6.4	278	2	B85807	hypothetical prote
78	76.5	6.4	282	2	H90958	hypothetical prote
79	76.5	6.4	352	2	H95869	probable sugar ABC
80	76.5	6.4	352	2	T25170	hypothetical prote
81	76.5	6.4	1450	2	T37258	cystic fibrosis tr
82	76.5	6.4	1783	2	C88728	probable voltage-d
83	76.5	6.4	1917	2	C88728	protein C4BA7.1 [i
84	76	6.4	156	2	I62107	melatonin receptor
85	76	6.4	263	2	G95198	hypothetical prote
86	76	6.4	263	2	C98065	hypothetical prote
87	76	6.4	339	2	E82211	conserved hypothet
88	76	6.4	352	2	H64919	hypothetical prote
89	76	6.4	352	2	B85769	probable membrane
90	76	6.4	669	2	C90921	hypothetical prote
91	76	6.4	402	2	C90921	NADH2 dehydrogenas
92	75.5	6.3	342	2	F91209	hypothetical prote
93	75.5	6.3	646	2	A86056	NADH2 dehydrogenas
94	75.5	6.3	538	2	A39412	hypothetical prote
95	75.5	6.3	494	2	S40689	conserved membrane
96	75.5	6.3	352	2	S40689	probable membrane
97	75.5	6.3	352	2	C90921	hypothetical prote
98	75.5	6.3	415	2	A86056	low affinity trypt
99	75.5	6.3	415	2	A39412	low affinity trypt
100	75.5	6.3	415	2	A86056	tryptophan transpo
101	75.5	6.3	471	2	S40689	5-hydroxytryptamin
102	75.5	6.3	498	2	T11039	NADH2 dehydrogenas

#					Accession	Description
103	75.5	6.3	593	2	H64594	multidrug resistan
104	75.5	6.3	708	2	T29669	hypothetical prote
105	75.5	6.3	775	2	T52107	anion channel prot
106	75.5	6.3	1142	2	T39103	probable negative
107	75	6.3	249	2	G64470	sulfate/thiosulfat
108	75	6.3	274	2	A82509	probable phosphati
109	75	6.3	330	2	B71163	probable oligopept
110	75	6.3	473	2	B38627	gamma-aminobutyric
111	75	6.3	526	2	T45850	hypothetical prote
112	75	6.3	649	2	C69810	anion-binding prot
113	75	6.3	753	2	H90124	hypothetical prote
114	75	6.3	2248	1	D42088	adenylate cyclase
115	74.5	6.2	276	2	A95881	probable trehalose
116	74.5	6.2	335	2	H72420	oligopeptide ABC t
117	74.5	6.2	355	2	JC4304	orphan G protein-c
118	74.5	6.2	471	2	A34863	serotonin receptor
119	74.5	6.2	473	2	B84143	Na+/H+ antiporter
120	74.5	6.2	500	2	T14826	transcription init
121	74.5	6.2	574	2	T05964	probable low-affin
122	74.5	6.2	618	1	S38000	probable transport
123	74.5	6.2	1808	1	T47792	hypothetical prote
124	.74	6.2	231	1	C69540	cobalamin (5'-phos
125	.74	6.2	231	2	B69422	quinone-reactive N
126	74	6.2	281	1	S26018	NADH2 dehydrogenas
127	74	6.2	286	2	S73424	spermidine/putresc
128	74	6.2	312	2	C72547	probable aspartate
129	74	6.2	312	2	H86732	hypothetical prote
130	74	6.2	349	2	JC6311	interferon recepto
131	74	6.2	350	2	I38848	Mel-la melatonin r
132	74	6.2	396	2	H89869	hypothetical prote
133	74	6.2	442	2	C86859	transmembrane effl
134	74	6.2	449	2	S02011	serotonin receptor
135	74	6.2	475	2	T36137	probable amino aci
136	74	6.2	485	2	T24115	hypothetical prote
137	73.5	6.2	487	1	S76713	cytochrome P450 d1
138	74	6.2	493	2	I40448	conserved hypothet
139	74	6.2	1123	1	JC7378	L-lysine 6-aminotr
140	73.5	6.2	153	2	T51517	telomerase reverse
141	73.5	6.2	192	2	E95845	conserved hypothet
142	73.5	6.2	216	1	A84727	hypothetical prote
143	73.5	6.2	216	2	G70474	hypothetical prote
144	73.5	6.2	318	2	S76713	hypothetical prote
145	73.5	6.2	338	2	I40448	conserved hypothet
146	73.5	6.2	379	2	S58448	ubiquinol-cytochro
147	73.5	6.2	384	2	AF0636	glucans biosynthes
148	73.5	6.2	385	1	S01511	ubiquinol-cytochro
149	73.5	6.2	385	2	A69804	ABC transporter (A
150	73.5	6.2	413	2	AD1738	Similar to multidr
151	73.5	6.2	442	2	C96672	hypothetical prote
152	73.5	6.2	491	1	EDBEM5	immediate-early pr
153	73.5	6.2	634	2	P82623	potassium uptake p
154	73.5	6.2	637	2	H83945	DNA mismatch repai
155	73.5	6.2	640	2	B32935	hypothetical prote
156	73.5	6.2	731	2	T31914	hypothetical prote
157	73.5	6.2	1095	2	E96744	probable oligopept
158	73.5	6.2	1174	2	A39927	RNA-directed RNA p
159	73	6.1	114	2	F71925	cag island protein
160	73	6.1	282	2	S26030	NADH2 dehydrogenas
161	73	6.1	339	2	T15560	hypothetical prote
162	73	6.1	450	1	WZBEE4	49.2K membrane pro
163	73	6.1	453	2	T30985	hypothetical prote
164	73	6.1	553	2	A71823	hypothetical prote
165	73	6.1	788	2	G89901	hypothetical prote
166	73	6.1	971	2	T00268	hypothetical prote
167	73	6.1	1075	2	B96508	hypothetical prote
168	72.5	6.1	6805	2	S20901	titin - rabbit (fr
169	72.5	6.1	209	2	S72929	hypothetical prote
170	72.5	6.1	222	2	B85866	probable transport
171	72.5	6.1	222	2	B91022	hypothetical prote
172	72.5	6.1	255	2	H64996	hypothetical prote
173	72.5	6.1	291	2	A60944	ubiquinol-cytochro
174	72.5	6.1	307	2	TO2986	chlorophyll a/b-bi
175	72.5	6.1	315	2	H96598	conserved hypothet / protein F20N2.8 [i
176	72.5	6.1	325	2	H86670	hypothetical prote
177	72.5	6.1	336	2	C88951	protein C38C3.2 (i
178	72.5	6.1	389	2	A55493	oxytocin receptor
179	72.5	6.1	428	2	AF0173	probable paraquat-
180	72.5	6.1	499	2	H70453	virulence factor M
181	72.5	6.1	513	2	S47631	pituitary adenylat
182	72.5	6.1	522	2	T29705	hypothetical prote
183	72.5	6.1	635	2	T23465	hypothetical prote
184	72.5	6.1	718	2	S57913	probable transloca
185	72.5	6.1	749	2	C84508	probable cap-bindi
186	72.5	6.1	1539	2	T30037	hypothetical prote
187	72	6.1	279	2	T21099	hypothetical prote
188	72	6.0	306	2	AE1156	probable permease
189	72	6.0	339	2	G97199	hypothetical prote
190	72	6.0	377	2	T27805	hypothetical prote
191	72	6.0	379	2	T11349	hypothetical prote
192	72	6.0	415	1	H70975	late L1 52K protei
193	72	6.0	415	2	WMAD65	late L1 52K protei
194	72	6.0	453	2	T39155	glycosyl hydrolase
195	72	6.0	453	2	D89760	conserved hypothet
196	72	6.0	479	2	S64587	DNA-directed DNA p
197	72	6.0	497	2	G96611	hypothetical prote
198	72	6.0	514	2	T15338	probable ethylene
199	72	6.0	594	2	T42660	hypothetical prote
200	72	6.0	600	2	T39873	hypothetical prote
201	72	6.0	630	2	T07966	probable cytochrom
202	72	6.0	1038	2	S37854	hypothetical prote
203	72	6.0	1094	2	S22573	trp protein - frui
204	72	6.0	1113	2	T20140	patched protein -
205	72	6.0	1220	2	T18291	P-glycoprotein 6 -
206	72	6.0	1275	2	JU0092	cytochrome-c oxida
207	72	6.0	1282	2	T30804	E1 membrane glycop
208	72	6.0	210	2	S52050	sensory transducti
209	71.5	6.0	225	1	MMIH68	prostaglandin E(2)
210	71.5	6.0	237	2	T07966	flagellar biosynth
211	71.5	6.0	246	2	AG3644	hypothetical prote
212	71.5	6.0	301	2	F86647	hypothetical prote
213	71.5	6.0	341	2	F90084	hypothetical prote
214	71.5	6.0	345	2	T33706	sensory transducti
215	71.5	6.0	348	2	D82252	EP3-alpha receptor
216	71.5	6.0	355	2	AB3516	Mel-1a melatonin r
217	71.5	6.0	362	2	S48689	Mel-1a melatonin r
218	71.5	6.0	366	2	S51280	ubiquinol-cytochro
219	71.5	6.0	366	2	I46469	hypothetical prote
220	71.5	6.0	381	2	T11776	hypothetical prote
221	71.5	6.0	383	2	T38194	isotocin receptor
222	71.5	6.0	390	1	S34043	oxytocin receptor
223	71.5	6.0	390	2	S64497	isotocin receptor
224	71.5	6.0	435	2	AD1340	maltodextrin ABC-t
225	71.5	6.0	435	2	AB1711	maltodextrin ABC-t
226	71.5	6.0	471	2	PS0154	125K surface antig
227	71.5	6.0	510	2	T10124	hexose transport p
228	71.5	6.0	524	2	T02499	hypothetical prote
229	71.5	6.0	603	2	H90061	hypothetical prote
230	71.5	6.0	651	2	T46050	betr protein homol
231	71.5	6.0	669	2	D64137	mediates transport
232	71.5	6.0	670	2	A49580	adenylate cyclase
233	71.5	6.0	823	2	T34472	genome polyprotein
234	71.5	6.0	1407	2	B42239	cag pathogenicity
235	71.5	6.0	3010	1	S18030	conserved hypothet
236	71	6.0	114	1	H64586	E1 membrane glycop
237	71	6.0	225	2	MMIHAI	conserved hypothet
238	71	6.0	250	2	A82367	probable processin
239	71	5.9	258	2	A81355	chlorophyll a/b-bi
240	71	5.9	290	2	S33443	hypothetical prote
241	71	5.9	339	2	T16745	hypothetical prote
242	71	5.9	345	2	T12372	NADH2 dehydrogenas
243	71	5.9	345	2	T25561	hypothetical prote
244	71	5.9	361	2	C90603	hypothetical prote
245	71	5.9	361	2	F86759	3-deoxy-D-manno-oc
246	71	5.9	391	2	F87286	transcription regu
247	71	5.9	423	2	AF1335	serotonin receptor
248	71	5.9	471	2	A43956	

#			Len	C	Accession	Description
249	71	5.9	546	2	S48932	hypothetical prote
250	71	5.9	563	2	T38766	probable transcrip
251	71	5.9	576	2	T22509	probable membrane
252	71	5.9	620	2	A58932	cytochrome C-type
253	71	5.9	676	2	E26725	hypothetical prote
254	71	5.9	788	2	E71813	probable cytochrom
255	71	5.9	913	2	T52485	probable component
256	71	5.9	2437	2	T18482	neurofilament prot
257	71	5.9	203	1	T31684	hypothetical prote
258	70.5	5.9	266	2	H98208	hypothetical prote
259	70.5	5.9	266	2	A13077	probable bacitraci
260	70.5	5.9	266	2	T41414	probable permease
261	70.5	5.9	279	2	AH2408	permease protein o
262	70.5	5.9	291	2	S22041	hypothetical prote
263	70.5	5.9	340	2	S76294	hypothetical prote
264	70.5	5.9	352	2	B90537	hypothetical prote
265	70.5	5.9	365	2	I38748	protaglandin recep
266	70.5	5.9	365	2	S51315	protaglandin E re
267	70.5	5.9	374	2	I38747	protaglandin recep
268	70.5	5.9	374	2	S51317	protaglandin E re
269	70.5	5.9	388	2	S51316	protaglandin E re
270	70.5	5.9	388	2	I38750	protaglandin E re
271	70.5	5.9	389	2	S71336	protaglandin recep
272	70.5	5.9	390	2	S43375	mesotocin receptor
273	70.5	5.9	393	2	S51313	protaglandin E re
274	70.5	5.9	393	2	S51318	protaglandin E re
275	70.5	5.9	423	1	E71065	hypothetical prote
276	70.5	5.9	425	2	S51319	protaglandin E re
277	70.5	5.9	472	2	AG3600	cellulose synthase
278	70.5	5.9	496	2	B64638	chitin synthase (E
279	70.5	5.9	521	2	E64181	hypothetical prote
280	70.5	5.9	548	2	A81650	conserved hypothet
281	70.5	5.9	556	2	T16790	hypothetical prote
282	70.5	5.9	574	2	S45754	probable membrane
283	70.5	5.9	598	2	F46027	gamma-aminobutyric
284	70.5	5.9	599	1	ACRTGT	gamma-aminobutyric
285	70.5	5.9	700	2	T10566	probable serine/th
286	70.5	5.9	766	2	T48463	hypothetical prote
287	70.5	5.9	1026	2	T18220	chitin synthase (E
288	70.5	5.9	1583	2	F97846	hypothetical prote
289	70.5	5.9	1787	2	T20160	hypothetical prote
290	70.5	5.9	5138	2	B96695	hypothetical prote
291	70	5.9	189	2	T51847	conserved hypothet
292	70	5.9	199	2	T08902	manganese-binding
293	70	5.9	213	2	F86310	protein FL13.8 [lim
294	70	5.9	256	2	T13597	hypothetical prote
295	70	5.9	287	2	T52317	hypothetical prote
296	70	5.9	292	2	H64244	chlorophyll a/b-bi
297	70	5.9	307	2	E95010	H+-transporting tw
298	70	5.9	307	2	B97882	ABC transporter, P
299	70	5.9	330	2	T30981	hypothetical prote
300	70	5.9	333	2	I38974	hypothetical prote
301	70	5.9	371	2	T46421	G protein-coupled
302	70	5.9	388	2	A55597	oxytocin receptor
303	70	5.9	416	2	A85112	probable ankyrin-r
304	70	5.9	418	2	T08882	proline/betaine tr
305	70	5.9	420	2	E72357	sugar ABC transpor
306	70	5.9	427	2	T01905	hypothetical prote
307	70	5.9	437	2	C91261	hypothetical prote
308	70	5.9	437	2	G86101	glutamate-aspartat
309	70	5.9	438	2	AF3215	glutamate-aspartat
310	70	5.9	450	2	T42595	ABC transporter, m
311	70	5.9	494	2	B89827	envelope protein 5
312	70	5.9	532	2	T49467	hypothetical prote
313	70	5.9	551	2	A87019	related to COP1-in
314	70	5.9	554	2	T27878	hypothetical prote
315	70	5.9	558	2	H72565	probable cytochrom
316	70	5.9	675	2	T22323	hypothetical prote
317	70	5.9	735	2	S46830	hypothetical prote
318	70	5.9	963	2	T26022	urea transport pro
319	70	5.9	1930	1	F86200	hypothetical prote
320	69.5	5.8	133	1	MNIHHC	nonstructural prot
321	69.5	5.8	206	2	S76279	hypothetical prote
322	69.5	5.8	285	2	F70194	hypothetical prote
323	69.5	5.8	321	2	S59388	probable membrane
324	69.5	5.8	339	2	A97736	hypothetical membrane
325	69.5	5.8	347	2	G90444	hypothetical prote
326	69.5	5.8	354	2	I58186	probable G protein
327	69.5	5.8	361	2	A53216	prostaglandin E re
328	69.5	5.8	362	2	S36766	prostaglandin E re
329	69.5	5.8	384	2	S62758	ubiquinol-cytochro
330	69.5	5.8	385	2	S36767	prostaglandin E re
331	69.5	5.8	387	2	T32561	hypothetical prote
332	69.5	5.8	394	2	AG1208	cell-division prot
333	69.5	5.8	400	2	S51791	Drosophila transio
334	69.5	5.8	402	2	B90986	probable colanic a
335	69.5	5.8	405	2	G64971	probable colanic a
336	69.5	5.8	405	2	H85831	Putative colanic a
337	69.5	5.8	411	2	B53216	prostaglandin E2 r
338	69.5	5.8	417	2	S36764	prostaglandin E re
339	69.5	5.8	421	2	G72300	conserved hypothet
340	69.5	5.8	436	2	T44832	prostaglandin E re
341	69.5	5.8	453	2	D98003	conserved hypothet
342	69.5	5.8	477	2	T25798	hypothetical prote
343	69.5	5.8	490	2	E82740	C4-dicarboxylate t
344	69.5	5.8	503	2	C86250	hypothetical prote
345	69.5	5.8	507	2	T50054	probable transport
346	69.5	5.8	515	2	E86534	ADP/ATP transloca
347	69.5	5.8	547	2	G86581	integral membrane
348	69.5	5.8	547	2	F72042	organic cation tra
349	69.5	5.8	557	2	JW0089	integral membrane
350	69.5	5.8	557	2	AC2137	organic cation tra
351	69.5	5.8	570	2	B96776	ABC transporter AT
352	69.5	5.8	570	2	D97337	hypothetical prote
353	69.5	5.8	579	2	AG1412	probable ATP-bindi
354	69.5	5.8	579	2	AF1788	ATP-binding casset
355	69.5	5.8	596	2	S11073	apolipoprotein B -
356	69.5	5.8	604	2	T31042	apolipoprotein B -
357	69.5	5.8	604	2	F84525	hypothetical prote
358	69.5	5.8	607	2	E84463	Mutator-like trans
359	69.5	5.8	616	2	S58824	Mutator-like trans
360	69.5	5.8	877	2	A58824	probable membrane
361	69.5	5.8	881	2	E83941	probable membrane
362	69.5	5.8	1704	2	AC2089	probable ATP-bindi
363	69.5	5.8	1704	2	S71363	ATP-binding casset
364	69.5	5.8	2629	2	A59188	uncharacterized me
365	69.5	5.8	7829	2	JT0382	apolipoprotein B -
366	69	5.8	169	2	T45569	hypothetical prote
367	69	5.8	169	2	T15789	hypothetical prote
368	69	5.8	244	2	H96934	hypothetical prote
369	69	5.8	244	2	A96998	hypothetical prote
370	69	5.8	256	2	C64145	hypothetical prote
371	69	5.8	261	2	T07481	hypothetical prote
372	69	5.8	273	2	F83805	hypothetical prote
373	69	5.8	273	2	C71707	melatonin receptor
374	69	5.8	289	2	S72554	probable sugar upt
375	69	5.8	291	2	D96002	hypothetical prote
376	69	5.8	300	2	D71424	O-antigen polymera
377	69	5.8	338	2	I69644	hypothetical prote
378	69	5.8	339	2	B69436	LSU ribosomal prot
379	69	5.8	345	2	AH1514	hypothetical prote
380	69	5.8	351	2	AD0273	probable integral
381	69	5.8	379	2	S58447	ubiquinol-cytochro
382	69	5.8	382	2	AI3175	conserved hypothet
383	69	5.8	382	2	D71424	hypothetical prote
384	69	5.8	384	2	H99979	hypothetical prote
385	69	5.8	436	2	T11268	hypothetical prote
386	69	5.8	437	2	A42384	transposase - Baci
387	69	5.8	443	2	T19512	glutamate-aspartat
388	69	5.8	478	2	S25821	hypothetical prote
389	69	5.8	478	2	T33985	NADH2 dehydrogenas
390	69	5.8	508	2	E96804	probable thioredox
391	69	5.8	523	2	T11916	hypothetical prote
392	69	5.8	540	2	T24675	NADH2 dehydrogenas
393	69	5.8	549	2	E70784	cytochrome b homol
394	69	5.8	579	2	A64100	inner membrane cop

Seq			Len	N	Code	Description
395	69	5.8	599	2	G90476	probable Na+/H+ an
396	69	5.8	600	2	T11889	NADH2 dehydrogenas
397	69	5.8	637	2	H96592	probable multispan
398	69	5.8	659	2	D84633	probable multispan
399	69	5.8	791	2	T12455	hypothetical prote
400	69	5.8	802	2	JH0595	potassium channel
401	69	5.8	863	2	H84490	hypothetical prote
402	69	5.8	933	2	AD3309	hypothetical membr
403	69	5.8	1058	2	T30580	P-type ATPase - sl
404	69	5.8	1344	2	T34188	myb-binding protei
405	69	5.8	1392	2	T01908	hypothetical prote
406	69	5.8	1515	2	T04204	hypothetical prote
407	69	5.8	3010	1	A45573	genome polyprotein
408	68.5	5.7	225	2	AE03371	probable carboxype
409	68.5	5.7	237	2	T25877	hypothetical prote
410	68.5	5.7	238	2	T04280	hypothetical prote
411	68.5	5.7	260	2	H75428	hypothetical prote
412	68.5	5.7	262	2	AG1830	hypothetical prote
413	68.5	5.7	265	2	AI3428	O-antigen export s
414	68.5	5.7	285	2	E86835	hypothetical prote
415	68.5	5.7	297	2	S74335	maltose ABC transp
416	68.5	5.7	304	2	AG3035	carbon dioxide con
417	68.5	5.7	304	2	D98250	hypothetical prote
418	68.5	5.7	343	2	AC2129	probable sugar ABC
419	68.5	5.7	359	2	B59105	iron(III) dicitrat
420	68.5	5.7	362	2	D72424	oligopeptide ABC t
421	68.5	5.7	377	1	JQ2337	omega-3 fatty acid
422	68.5	5.7	383	2	I53870	Edg-1 orphan recep
423	68.5	5.7	391	2	H81265	probable transmemb
424	68.5	5.7	395	2	B83774	probable transmemb
425	68.5	5.7	395	2	A96189	hypothetical prote
426	68.5	5.7	395	2	AH3097	conserved hypothet
427	68.5	5.7	419	2	AG1660	multidrug resistan
428	68.5	5.7	420	2	I51666	Mel-1c receptor su
429	68.5	5.7	425	2	F97108	probable glycosylt
430	68.5	5.7	430	2	S15308	hypothetical prote
431	68.5	5.7	431	2	H72247	preprotein translo
432	68.5	5.7	444	2	A48260	corticoliberin rec
433	68.5	5.7	445	2	E22845	hypothetical prote
434	68.5	5.7	479	2	T44326	hypothetical prote
435	68.5	5.7	480	2	B70446	hypothetical prote
436	68.5	5.7	488	2	T15941	hypothetical prote
437	68.5	5.7	492	2	G90574	NADH2 dehydrogenas
438	68.5	5.7	502	2	S77331	hypothetical prote
439	68.5	5.7	512	2	T00605	probable cytochrom
440	68.5	5.7	518	2	S50465	PAC2 protein - yea
441	68.5	5.7	525	2	JN0902	pituitary adenylat
442	68.5	5.7	542	2	S58102	hypothetical prote
443	68.5	5.7	558	2	F64235	Na+ ATPase chain J
444	68.5	5.7	634	2	C83530	probable ABC trans
445	68.5	5.7	670	2	G86702	potassium uptake p
446	68.5	5.7	724	2	H86427	potassium uptake p
447	68.5	5.7	788	2	G64707	unknown protein [i
448	68.5	5.7	923	1	MMBY7C	cation-transportin
449	68.5	5.7	1004	2	S55353	probable membrane
450	68.5	5.7	146	2	H75201	probable copper-tr
451	68.5	5.7	205	2	A64373	hypothetical prote
452	68.5	5.7	255	2	F39925	hypothetical prote
453	68	5.7	266	2	C95316	probable ABC trans
454	68	5.7	270	2	AE3627	maltose transport
455	68	5.7	279	2	AG2165	bicarbonate transp
456	68	5.7	294	2	T41953	G protein-coupled
457	68	5.7	294	2	AE0004	ribonuclease BN (E
458	68	5.7	313	2	B38888	COI intron 9 re
459	68	5.7	355	2	A45177	chemokine (C-C) re
460	68	5.7	360	2	T11067	ubiquinol-cytochro
461	68	5.7	364	2	JC2115	prostaglandin E re
462	68	5.7	365	2	JN0693	prostaglandin E2 r
463	68	5.7	370	2	H90559	hypothetical prote
464	68	5.7	379	2	S61040	ubiquinol-cytochro
465	68	5.7	393	2	AG0184	probable multidrug
466	68	5.7	402	2	T41253	hypothetical wf5
467	68	5.7	417	2	T11387	NADH2 dehydrogenas
468	68	5.7	426	2	C69831	conserved hypothet
469	68	5.7	464	2	C70414	NADH2 dehydrogenas
470	68	5.7	473	2	H71044	hypothetical prote
471	68	5.7	475	2	E83450	cytochrome-c oxida
472	68	5.7	477	2	H91123	probable oxidoredu
473	68	5.7	477	2	G85968	probable oxidoredu
474	68	5.7	477	2	C65096	hypothetical 52.1
475	68	5.7	502	1	A53572	prostaglandin E2 r
476	68	5.7	519	1	I30010	NADH2 dehydrogenas
477	68	5.7	519	2	T39918	prostaglandin E2 r
478	68	5.7	542	2	A69261	probable acetyl-co
479	68	5.7	542	2	B81910	probable acid-CoA
480	68	5.7	542	2	B81105	probable ABC-trans
481	68	5.7	620	2	T19907	ABC transporter, A
482	68	5.7	664	2	C84869	hypothetical prote
483	68	5.7	718	2	E83718	probable receptor
484	68	5.7	804	2	T49975	conserved hypothet
485	68	5.7	836	2	T18460	hypothetical prote
486	68	5.7	859	2	S69700	hypothetical prote
487	68	5.7	871	2	H72597	hypothetical prote
488	68	5.7	1429	2	T19422	hypothetical prote
489	68	5.7	1878	2	B86189	hypothetical prote
490	68	5.7	3010	1	GNWVTC	genome polyprotein
491	67.5	5.6	104	2	T36801	G protein-coupled
492	67.5	5.6	200	2	H72295	conserved hypothet
493	67.5	5.6	273	2	A97700	hypothetical prote
494	67.5	5.6	288	2	F72219	conserved hypothet
495	67.5	5.6	320	2	T23674	hypothetical prote
496	67.5	5.6	323	2	QOBED1	HHRF3 protein - hu
497	67.5	5.6	348	1	T12591	NADH2 dehydrogenas
498	67.5	5.6	354	2	T09353	G protein-coupled
499	67.5	5.6	387	2	T24581	protein TllF1.1 [i
500	67.5	5.6	397	2	T08086	protein TllF1.1 [i
501	67.5	5.6	419	2	A83999	hypothetical prote
502	67.5	5.6	439	2	AH1288	mutants block spor
503	67.5	5.6	450	2	H83699	multidrug resistan
504	67.5	5.6	450	2	G91219	sodium-dependent c
505	67.5	5.6	450	2	G86026	sodium-dependent c
506	67.5	5.6	452	2	F65183	TDP-Fuc4NAc lipidI
507	67.5	5.6	459	2	G89870	TDP-Fuc4NAc lipidI
508	67.5	5.6	462	2	JH0594	4-alpha-1-fucosylt
509	67.5	5.6	483	2	G84113	hypothetical prote
510	67.5	5.6	488	1	OXASM4	vasoactive intesti
511	67.5	5.6	492	2	T28500	hypothetical prote
512	67.5	5.6	498	2	T48262	NADH2 dehydrogenas
513	67.5	5.6	515	2	F64464	sodium-dependent n
514	67.5	5.6	515	2	T48262	hypothetical prote
515	67.5	5.6	598	2	H82973	hypothetical prote
516	67.5	5.6	632	2	B72089	ADP, ATP carrier P
517	67.5	5.6	676	1	I51368	choline transporte
518	67.5	5.6	676	2	I71259	gamma-aminobutyric
519	67.5	5.6	676	2	WZV218	probable dicarboxy
520	67.5	5.6	676	1	T37345	vacuolar ATPase (E
521	67.5	5.6	676	2	D42511	hypothetical prote
522	67.5	5.6	676	2	F36843	hypothetical prote
523	67.5	5.6	682	2	T28500	NPH-II, helicase -
524	67.5	5.6	686	2	D72158	I8 protein - vacci
525	67.5	5.6	716	2	G89870	I8R protein - vacc
526	67.5	5.6	740	1	H82973	ATP/GTP-binding pr
527	67.5	5.6	838	2	G82448	ATP/GTP-binding pr
528	67.5	5.6	866	2	S30687	hypothetical prote
529	67.5	5.6	950	2	G82448	L8R protein - vari
530	67.5	5.6	1159	2	S30687	sensor histidine k
531	67.5	5.6	1244	2	T02567	hypothetical prote
532	67.5	5.6	1411	2	T02866	probable ATP-bindi
533	67.5	5.6	1753	2	T19615	probable ATP-bindi
534	67.5	5.6	2332	1	S48442	hypothetical prote
535	67	5.6	151	2	S30855	hypothetical prote
536	67	5.6	151	2	T20574	conserved hypothet
537	67	5.6	159	2	A72093	genome polyprotein
538	67	5.6	159	2	H86529	conserved hypothet
539	67	5.6	180	2	S61040	CT101 hypothetical
540	67	5.6	203	2	I48129	probable membrane
	67	5.6	225	1	D70150	Xe169 (escapes X-i
	67	5.6	225	2	MMIHIB	probable membrane
	67	5.6	244	2	D70404	B1 membrane glycop
						conserved hypothet

No.					Code	Description
541	67	5.6	255	2	C50078	hypothetical prote
542	67	5.6	275	2	G98194	sugar ABC transpor
543	67	5.6	275	2	AC3092	hypothetical prote
544	67	5.6	275	2	S75698	hypothetical prote
545	67	5.6	276	2	F69307	conserved hypothet
546	67	5.6	276	2	S35270	DNA-damage repair
547	67	5.6	283	2	F96959	tRNA-processing ri
548	67	5.6	285	2	AE3024	hypothetical prote
549	67	5.6	286	2	D64235	hypothetical prote
550	67	5.6	314	2	D96703	hypothetical prote
551	67	5.6	317	2	D98260	inner membrane pro
552	67	5.6	336	2	A96997	ferrichrome transp
553	67	5.6	345	2	T21776	hypothetical prote
554	67	5.6	349	2	D84167	hypothetical prote
555	67	5.6	350	2	C88987	protein C50H11.2 [
556	67	5.6	352	2	T32314	hypothetical prote
557	67	5.6	379	2	S58451	ubiquinol-cytochro
558	67	5.6	379	2	S58449	ubiquinol-cytochro
559	67	5.6	396	1	C69291	pheromone shutdown
560	67	5.6	407	2	E70309	hypothetical prote
561	67	5.6	411	2	B71500	probable amino aci
562	67	5.6	415	2	S74041	pyruvate synthase
563	67	5.6	416	2	T46401	hypothetical prote
564	67	5.6	423	2	C95085	sodium-dependent t
565	67	5.6	436	2	AC1021	proton glutamate s
566	67	5.6	441	2	F86279	hypothetical prote
567	67	5.6	446	2	G72287	hypothetical prote
568	67	5.6	496	2	A31986	glucose transporte
569	67	5.6	507	2	AB1707	glycine betaine tr
570	67	5.6	516	2	AE0665	probable membrane
571	67	5.6	646	2	JC7777	ATP binding casset
572	67	5.6	717	2	T49238	hypothetical prote
573	67	5.6	753	2	S58331	dolichyl-phosphate
574	67	5.6	769	2	F81415	DNA topoisomerase
575	67	5.6	784	2	C82679	cell division prot
576	67	5.6	787	2	PN0677	hypothetical prote
577	67	5.6	798	2	T34248	probable serine/th
578	67	5.6	814	2	T05537	probable integral
579	67	5.6	823	2	T35280	conserved hypothet
580	67	5.6	880	2	D69427	probable NADH dehy
581	67	5.6	891	2	B82495	galactosamine-cont
582	67	5.6	900	2	E69631	chitin synthase (E
583	67	5.6	1175	2	S39951	DNA-directed DNA p
584	67	5.6	1242	1	DJBEC1	probable membrane
585	67	5.6	1333	2	S63403	pleiotropic drug r
586	67	5.6	1511	1	A53151	conserved hypothet
587	67	5.6	1575	2	G82905	hypothetical prote
588	67	5.6	1879	2	T19481	hypothetical prote
589	67	5.6	1905	2	T18267	sodium channel SCA
590	67	5.6	1993	1	T30902	multidrug resistan
591	67	5.6	3010	1	GNMVCJ	genome polyprotein
592	66.5	5.6	153	1	G69847	conserved hypothet
593	66.5	5.6	203	2	T28732	hypothetical prote
594	66.5	5.6	204	2	S70876	ABC transporter, P
595	66.5	5.6	218	2	S77103	hypothetical prote
596	66.5	5.6	245	2	A81405	sec-independant pr
597	66.5	5.6	263	2	AI2384	hypothetical prote
598	66.5	5.6	268	2	A70417	conserved hypothet
599	66.5	5.6	272	1	AI0075	hypothetical prote
600	66.5	5.6	279	1	S56642	nitrate transport
601	66.5	5.6	279	2	E70322	hypothetical prote
602	66.5	5.6	293	2	A84110	sugar ABC transpor
603	66.5	5.6	316	2	C70506	hypothetical prote
604	66.5	5.6	333	2	P81712	ABC transporter, P
605	66.5	5.6	347	2	AD2201	hypothetical prote
606	66.5	5.6	356	2	T20737	hypothetical prote
607	66.5	5.6	359	2	P90055	conserved hypothet
608	66.5	5.6	367	2	S75836	hypothetical prote
609	66.5	5.6	367	2	G89786	hypothetical prote
610	66.5	5.6	380	2	G89786	hypothetical prote
611	66.5	5.6	384	1	I38890	hypothetical prote
612	66.5	5.6	389	2	E96516	dual specificity p
613	66.5	5.6	400	2	G00013	F16N3.13 [imported
614	66.5	5.6	412	2	G89773	hypothetical prote
615	66.5	5.6	413	2	H95041	polysaccharide tra
616	66.5	5.6	435	2	D98111	hypothetical prote
617	66.5	5.6	435	2	G95246	maltodextrin ABC t
618	66.5	5.6	453	2	B95135	MATE efflux family
619	66.5	5.6	462	2	H71228	hypothetical prote
620	66.5	5.6	488	2	G71969	cytochrome-c oxida
621	66.5	5.6	488	2	D84998	hypothetical prote
622	66.5	5.6	490	2	A46391	low-affinity inorg
623	66.5	5.6	491	2	AC1555	cAMP receptor subt
624	66.5	5.6	493	2	A71875	efflux transporter
625	66.5	5.6	494	2	T32644	hypothetical prote
626	66.5	5.6	507	2	T27627	nickel transport s
627	66.5	5.6	539	2	G83720	hypothetical prote
628	66.5	5.6	547	2	B91135	probable alkaline
629	66.5	5.6	547	2	H85980	probable alkaline
630	66.5	5.6	550	1	A48026	sterol O-acyltrans
631	66.5	5.6	582	2	C71424	hypothetical prote
632	66.5	5.6	583	2	AI1510	C-terminal domain
633	66.5	5.6	598	2	T32430	hypothetical prote
634	66.5	5.6	663	2	AG2696	cytochrome c-type
635	66.5	5.6	663	2	G97478	cytochrome c-type
636	66.5	5.6	727	2	I56506	Na+/Cl(-)-dependen
637	66.5	5.6	727	2	S27043	neurotransmitter t
638	66.5	5.6	782	2	S19876	genome polyprotein
639	66.5	5.6	862	2	B36786	hypothetical prote
640	66.5	5.6	889	2	T47311	hypothetical prote
641	66.5	5.6	992	2	T27479	hypothetical prote
642	66.5	5.6	1014	2	T31433	hypothetical prote
643	66.5	5.6	1083	2	C88854	protein F11A10.3 [
644	66.5	5.6	1144	2	H81037	DNA polymerase III
645	66.5	5.6	1456	2	T15961	hypothetical prote
646	66.5	5.6	1684	2	JW0057	gravin - human
647	66.5	5.6	1768	2	B85062	genome polyprotein
648	66.5	5.6	2151	1	S16449	genome polyprotein
649	66.5	5.6	2285	1	G02434	DNA-directed DNA p
650	66.5	5.6	2833	2	A43360	inositol 1,4,5-tri
651	66.5	5.6	3011	1	GNMVC3	genome polyprotein
652	66	5.6	93	2	S28759	NADH2 dehydrogenas
653	66	5.6	130	2	D83820	diacylglycerol kin
654	66	5.6	209	2	A89801	conserved hypothet
655	66	5.6	276	2	H96816	hypothetical prote
656	66	5.6	279	2	S42125	hypothetical prote
657	66	5.6	285	2	D87447	sulfate ABC transp
658	66	5.6	302	2	A99074	hypothetical prote
659	66	5.6	305	2	I47040	sterol O-acyltrans
660	66	5.6	317	1	B41671	iron transport pro
661	66	5.6	318	2	B84291	iron transport pro
662	66	5.6	322	2	B71137	hypothetical prote
663	66	5.6	332	2	C97272	conserved membrane
664	66	5.6	370	2	I52315	G protein-coupled
665	66	5.6	379	1	S17405	ubiquinol-cytochro
666	66	5.6	379	1	T31409	ubiquinol-cytochro
667	66	5.6	379	2	S58460	ubiquinol-cytochro
668	66	5.6	381	2	A35300	G protein-coupled
669	66	5.5	390	1	QOBET9	protein Ut33 - hum
670	66	5.5	397	2	T21154	protein Ut33 - hum
671	66	5.5	397	2	T44477	hypothetical prote
672	66	5.5	397	2	B70505	hypothetical prote
673	66	5.5	401	2	T44831	probable emulsan r
674	66	5.5	404	1	B64927	probable sugar tra
675	66	5.5	404	2	A85777	probable transport
676	66	5.5	404	2	E90928	probable transport
677	66	5.5	411	2	H86539	CBS domain protein
678	66	5.5	412	2	A82444	GGDEF family prote
679	66	5.5	418	2	T41027	hypothetical prote
680	66	5.5	418	2	B72353	hypothetical prote
681	66	5.5	424	2	T07366	probable phosphati
682	66	5.5	436	2	T14816	hypothetical prote
683	66	5.5	447	2	T18633	hypothetical prote
684	66	5.5	447	2	T37223	hypothetical prote
685	66	5.5	450	2	A38316	alpha-2B-adrenergi
686	66	5.5	453	2	P86846	alpha-2-adrenergic

SEQ	A	B	Length	N	Accession	Description
687	66	5.5	483	2	S75369	hypothetical prote
688	66	5.5	484	2	T24238	hypothetical prote
689	66	5.5	496	2	E82940	hypothetical prote
690	66	5.5	508	2	G47677	hypothetical prote
691	66	5.5	525	2	T28306	ORF MSV145 hypothe
692	66	5.5	527	2	G69635	PTS arbutin-like e
693	66	5.5	532	2	G90037	hypothetical prote
694	66	5.5	546	2	A69890	hypothetical prote
695	66	5.5	548	2	B87423	cytochrome-c oxida
696	66	5.5	552	2	S45886	hypothetical prote
697	66	5.5	565	2	S73707	Na(+) translocatin
698	66	5.5	570	2	S07744	hypothetical prote
699	66	5.5	573	1	S33212	NADH2 dehydrogenas
700	66	5.5	573	2	AF1418	INDAI protein - fu
701	66	5.5	573	2	AH1793	ABC transporter, A
702	66	5.5	619	2	T11314	ABC transporter, A
703	66	5.5	632	2	T24405	NADH2 dehydrogenas
704	66	5.5	654	2	A98350	hypothetical ABC t
705	66	5.5	654	2	AF2932	hypothetical prote
706	66	5.5	705	2	T48464	hypothetical prote
707	66	5.5	721	2	A70764	probable 9lgX prot
708	66	5.5	736	2	G01522	acidic 82 kDa prot
709	66	5.5	784	2	B90442	tricorn proteinase
710	66	5.5	1039	2	S76747	hypothetical prote
711	66	5.5	1054	2	A61221	probable calcium t
712	66	5.5	1359	2	T34036	hypothetical prote
713	66	5.5	1375	2	S48375	hypothetical prote
714	66	5.5	2599	2	F90608	hypothetical prote
715	66	5.5	26926	1	I38344	titin, cardiac mus
716	65.5	5.5	132	2	A97760	signal sequence pe
717	65.5	5.5	132	2	E83792	phosphate ABC tran
718	65.5	5.5	146	1	G69447	hypothetical prote
719	65.5	5.5	171	2	AI3476	signal peptidase I
720	65.5	5.5	197	2	I17106	hypothetical prote
721	65.5	5.5	210	2	T43100	signal sequence pe
722	65.5	5.5	252	2	F69456	hypothetical prote
723	65.5	5.5	290	2	F86839	NADH2 dehydrogenas
724	65.5	5.5	297	2	G99447	endoplasmic reticu
725	65.5	5.5	297	2	E70074	hypothetical prote
726	65.5	5.5	301	2	T21308	hypothetical prote
727	65.5	5.5	317	2	S23459	polysulfide reduct
728	65.5	5.5	327	2	T36087	probable binding p
729	65.5	5.5	348	1	S36003	NADH2 dehydrogenas
730	65.5	5.5	351	2	B82880	hypothetical prote
731	65.5	5.5	365	1	F69629	NADH2 dehydrogenas
732	65.5	5.5	367	2	JC2056	spore germination
733	65.5	5.5	379	2	S58456	prostaglandin E2 r
734	65.5	5.5	379	2	T32778	ubiquinol-cytochro
735	65.5	5.5	391	2	T32601	NADH2 dehydrogenas
736	65.5	5.5	394	2	AH0362	hypothetical prote
737	65.5	5.5	410	2	T11064	nucleoside permeas
738	65.5	5.5	423	2	B82880	NADH2 dehydrogenas
739	65.5	5.5	425	2	A97688	conserved hypothet
740	65.5	5.5	425	2	AF2913	hypothetical prote
741	65.5	5.5	429	2	T32832	hypothetical prote
742	65.5	5.5	442	2	A42670	conserved hypothet
743	65.5	5.5	445	2	T38916	microfibril-associ
744	65.5	5.5	449	2	H83629	probable dicarboxy
745	65.5	5.5	457	2	A75327	probable transcrip
746	65.5	5.5	477	2	B75170	hypothetical prote
747	65.5	5.5	480	2	A60043	endoplasmic reticu
748	65.5	5.5	487	1	A97928	type I site-specif
749	65.5	5.5	488	2	H64537	cytochrome-c oxida
750	65.5	5.5	488	2	G81295	cytochrome-c oxida
751	65.5	5.5	491	2	AE1197	efflux transporter
752	65.5	5.5	495	2	A97022	probably membrane
753	65.5	5.5	500	2	G84706	hypothetical prote
754	65.5	5.5	502	2	AD3395	hypothetical prote
755	65.5	5.5	518	2	T25669	NADH2 dehydrogenas
756	65.5	5.5	528	2	A53207	hypothetical prote
757	65.5	5.5	534	2	T34417	probable folate tr
758	65.5	5.5	544	2	B84825	probable ABC trans
759	65.5	5.5	545	2	E90460	hypothetical prote
760	65.5	5.5	561	2	S71189	Dwarf1 protein - A
761	65.5	5.5	578	2	AH1417	ABC transporter (A
762	65.5	5.5	578	2	T15736	hypothetical prote
763	65.5	5.5	583	2	AH1151	glycerophosphory1
764	65.5	5.5	590	2	C81116	probable sugar epi
765	65.5	5.5	597	2	B82881	hypothetical prote
766	65.5	5.5	617	2	AB1167	phosphotransferase
767	65.5	5.5	618	2	ACI204	phosphotransferase
768	65.5	5.5	642	2	H70331	ATP-dependent heli
769	65.5	5.5	718	2	A56851	Na+/myo-inositol c
770	65.5	5.5	720	2	B82198	RTX toxin transpor
771	65.5	5.5	721	2	AF1254	penicillin-binding
772	65.5	5.5	740	2	S61568	probable membrane
773	65.5	5.5	860	1	QRHULD	LDL receptor precu
774	65.5	5.5	958	2	AC0204	probable integral
775	65.5	5.5	1087	2	S41797	cellulose 1,4-beta
776	65.5	5.5	1328	2	B22999	TyB protein - yea
777	65.5	5.5	1427	2	S74293	SRB8 protein - yea
778	65.5	5.5	1581	2	B71636	hypothetical prote
779	65.5	5.5	1635	2	T32452	hypothetical prote
780	65.5	5.4	126	2	AD0340	probable membrane
781	65.5	5.4	149	2	E89950	transcription regu
782	65.5	5.4	176	2	C69393	nitrate transport
783	65.5	5.4	196	2	Q1AD25	early E1B 21K prot
784	65.5	5.4	225	1	S40728	hypothetical prote
785	65.5	5.4	247	2	MMIHIV	E1 membrane glycop
786	65.5	5.4	257	2	I48149	serotonin receptor
787	65.5	5.4	259	2	B75099	hypothetical prote
788	65.5	5.4	271	2	A47112	growth response pr
789	65.5	5.4	280	2	H75068	hema concentration
790	65.5	5.4	290	2	S75957	nitrate transport
791	65.5	5.4	290	1	T02877	probable chloropy
792	65.5	5.4	291	2	C97453	cytochrome c oxida
793	65.5	5.4	307	2	AE2671	cytochrome c oxida
794	65.5	5.4	313	2	B36125	branched-chain ami
795	65.5	5.4	319	2	A64084	lysophospholipase
796	65.5	5.4	322	2	D87087	hypothetical prote
797	65.5	5.4	330	2	S38091	hypothetical prote
798	65.5	5.4	335	2	T15249	dipeptide abc tran
799	65.5	5.4	338	2	H69785	mannan endo-1,4-be
800	65.5	5.4	344	2	AD1200	NADH2 dehydrogenas
801	65.5	5.4	345	2	T12361	conserved hypothet
802	65.5	5.4	355	2	G70200	hypothetical prote
803	65.5	5.4	359	2	D34285	hypothetical prote
804	65.5	5.4	362	2	T11138	ubiquinol-cytochro
805	65.5	5.4	375	2	C84984	ubiquinol-cytochro
806	65.5	5.4	379	1	I38879	corticotropin rele
807	65.5	5.4	379	2	S17414	ubiquinol-cytochro
808	65.5	5.4	379	2	S58461	ubiquinol-cytochro
809	65.5	5.4	379	2	S58455	ubiquinol-cytochro
810	65.5	5.4	382	1	D34285	ubiquinol-cytochro
811	65.5	5.4	382	2	T11138	hypothetical prote
812	65.5	5.4	390	2	C84984	hypothetical prote
813	65.5	5.4	415	2	B81410	probable integral
814	65.5	5.4	438	2	A83122	probable MFS trans
815	65.5	5.4	442	2	AD2358	glucosyltransferas
816	65.5	5.4	445	2	T28334	Ser/Thr protein ki
817	65.5	5.4	457	2	B88613	protein T2E9.5 li
818	65.5	5.4	462	2	S54508	probable membrane
819	65.5	5.4	477	2	A69036	TRK system potassi
820	65.5	5.4	479	2	E81050	cytochrome-c oxida
821	65.5	5.4	481	2	T14545	probable sugar tra
822	65.5	5.4	492	2	S59107	NADH2 dehydrogenas
823	65	5.4	510	2	S55204	hypothetical prote
824	65	5.4	511	2	H75097	polysaccharide bio
825	65	5.4	513	2	T37180	probable membrane
826	65	5.4	526	2	D91047	hydrogenase 4 memb
827	65	5.4	530	2	A64697	hypothetical prote
828	65	5.4	530	2	B89771	conserved hypothet
829	65	5.4	535	2	S55190	hypothetical prote
830	65	5.4	539	2	T31543	SNG1 protein - yea
831	65	5.4	547	2	S53920	hypothetical prote
832	65	5.4	576	2	T25375	hypothetical prote

No.	Score		Len	N	ID	Description
833	65	5.4	579	2	S61131	probable membrane
834	65	5.4	608	2	S65298	dicarboxylic amino
835	65	5.4	611	2	T21747	probable amino
836	65	5.4	624	2	G82508	hypothetical prote
837	65	5.4	627	2	T11125	NADH2 dehydrogenas
838	65	5.4	633	2	F84483	NADH2 dehydrogenas
839	65	5.4	638	2	D69957	Mutator-like trans
840	65	5.4	643	2	F97787	conserved hypothet
841	65	5.4	676	2	A45515	sodium/pantothenat
842	65	5.4	684	2	F86394	dnaK-type molecula
843	65	5.4	697	2	H84791	protein T24P13.20
844	65	5.4	702	2	T13505	hypothetical prote
845	65	5.4	705	2	TO4400	NADH2 dehydrogenas
846	65	5.4	773	2	H96818	hypothetical prote
847	65	5.4	773	2	G83816	late competence op
848	65	5.4	808	2	TO4459	hypothetical prote
849	65	5.4	861	2	S77086	hypothetical prote
850	65	5.4	927	2	T38518	ribonuclease II RN
851	65	5.4	931	2	F84637	probable plasma me
852	65	5.4	938	2	TO1809	hypothetical prote
853	65	5.4	1089	2	C70522	hypothetical prote
854	65	5.4	1163	2	D64315	probable mmpL8 pro
855	65	5.4	1178	2	S76370	type I restriction
856	65	5.4	1232	2	I38496	anion exchanger 3
857	65	5.4	1421	2	T34225	sensory transducti
858	65	5.4	5069	2	T17464	rifamycin polyketi
859	64.5	5.4	180	2	T41339	hypothetical prote
860	64.5	5.4	211	2	S35280	eaC protein - phag
861	64.5	5.4	217	2	AE0395	probable amino aci
862	64.5	5.4	227	2	C69432	hypothetical prote
863	64.5	5.4	234	2	B96957	HAD superfamily hy
864	64.5	5.4	268	2	AF2470	potassium channel
865	64.5	5.4	271	2	E81384	prolipoprotein dia
866	64.5	5.4	275	2	T43119	hypothetical prote
867	64.5	5.4	293	2	D71517	probable metal tra
868	64.5	5.4	295	2	T32202	hypothetical prote
869	64.5	5.4	297	2	T27584	hypothetical prote
870	64.5	5.4	320	2	T23904	protein F3M18.6 [l
871	64.5	5.4	326	2	A86411	hypothetical prote
872	64.5	5.4	353	2	F64175	hypothetical prote
873	64.5	5.4	358	2	T22823	hypothetical prote
874	64.5	5.4	361	2	A86841	hypothetical prote
875	64.5	5.4	361	2	S43264	Pas (passover) pro
876	64.5	5.4	379	2	A40734	ubiquinol-cytochro
877	64.5	5.4	379	1	T11505	ubiquinol-cytochro
878	64.5	5.4	379	2	S58454	ubiquinol-cytochro
879	64.5	5.4	379	2	A53077	ubiquinol-cytochro
880	64.5	5.4	381	1	CBMS	pituitary adenylat
881	64.5	5.4	381	2	S33449	hypothetical prote
882	64.5	5.4	385	2	H69154	probable maltodext
883	64.5	5.4	398	2	H95057	NADH2 dehydrogenas
884	64.5	5.4	398	2	A97927	hypothetical prote
885	64.5	5.4	400	2	G01977	phosphoglycerate k
886	64.5	5.4	411	2	G46800	d3 dopamine recept
887	64.5	5.4	416	2	AF1127	LAG1 protein - yea
888	64.5	5.4	426	1	T45800	rod shape-determin
889	64.5	5.4	433	2	T11162	UDP-N-acetylglucos
890	64.5	5.4	435	2	AC0105	NADH2 dehydrogenas
891	64.5	5.4	439	2	C22845	probable maltdext
892	64.5	5.4	439	2	A84153	hypothetical prote
893	64.5	5.4	443	2	DYRTD3	hypothetical prote
894	64.5	5.4	444	2	T11474	NADH2 dehydrogenas
895	64.5	5.4	444	2	A43676	P44 hepatitis-asso
896	64.5	5.4	444	1	S48218	microtubular aggre
897	64.5	5.4	446	2	D85362	dopamine receptor
898	64.5	5.4	448	2	B26696	hypothetical prote
899	64.5	5.4	448	2	S57909	hypothetical prote
900	64.5	5.4	450	2	T23528	probable histidine
901	64.5	5.4	451	2	D70045	hypothetical prote
902	64.5	5.4	467	2	JN0616	two-component sens
903	64.5	5.4	478	2	C29051	pituitary adenylat
904	64.5	5.4	495	1	FWSYG2	transposase C - Ba
905	64.5	5.4	495	2	S39061	glycinin chain Ala
906	64.5	5.4	495	2	S36114	pituitary adenylyl
907	64.5	5.4	495	2	S10851	glycinin G1 precur
908	64.5	5.4	512	2	H64964	probable membrane
909	64.5	5.4	521	2	A99549	amino acid permeas
910	64.5	5.4	523	2	S39061	pituitary adenylyl
911	64.5	5.4	547	2	H65107	hypothetical prote
912	64.5	5.4	554	2	A56730	cat1 protein - Pod
913	64.5	5.4	554	2	B97812	virulence factor m
914	64.5	5.4	575	2	A81793	ABC transporter (A
915	64.5	5.4	576	2	AB1793	cytochrome P450 97
916	64.5	5.4	614	2	T05904	hypothetical prote
917	64.5	5.4	622	2	B99869	acyltransferase (t
918	64.5	5.4	638	2	AC1236	mRNA maturase b14
919	64.5	5.4	638	1	QOBY2M	hypothetical prote
920	64.5	5.4	715	2	T26307	hypothetical prote
921	64.5	5.4	720	2	T47648	ABC transporter-li
922	64.5	5.4	721	2	AD1617	penicillin-binding
923	64.5	5.4	721	2	AE1491	hypothetical prote
924	64.5	5.4	735	2	AD0341	probable membrane
925	64.5	5.4	763	2	AD1070	phosphatidylglycer
926	64.5	5.4	801	2	A89862	Na+/H+ antiporter
927	64.5	5.4	803	2	H64568	histidine kinase -
928	64.5	5.4	889	2	A70848	probable major cor
929	64.5	5.4	979	2	A70846	probable membrane
930	64.5	5.4	1007	2	B70723	125K protein - Clo
931	64.5	5.4	1114	2	JH0284	138K protein - Tet
932	64.5	5.4	1154	2	T48829	probable membrane
933	64.5	5.4	1465	2	S45628	related to SRBP c
934	64.5	5.4	1529	2	S69688	DNA-directed DNA p
935	64.5	5.4	1630	2	S64403	hypothetical prote
936	64.5	5.4	1661	2	S64800	ESP1 protein - yea
937	64.5	5.4	3033	1	GNWVJ8	probable membrane
938	64	5.4	202	2	A70041	genome polyprotein
939	64	5.4	209	2	G82359	conserved hypothet
940	64	5.4	253	2	JC5347	conserved hypothet
941	64	5.4	259	2	T12451	cdd3 protein - Clo
942	64	5.4	269	2	H69768	hypothetical prote
943	64	5.4	270	2	F89632	probable ABC-type
944	64	5.4	274	2	T50567	plant-metabolite d
945	64	5.4	276	2	C70040	conserved hypothet
946	64	5.4	276	2	C95932	probable F1326.3 [l
947	64	5.4	281	2	D83009	probable permease
948	64	5.4	283	2	B83883	probable sugar upt
949	64	5.4	285	2	S36955	sugar transport sy
950	64	5.4	288	2	T29675	cytochrome-c oxida
951	64	5.4	288	2	A48258	hypothetical prote
952	64	5.4	330	2	T11248	ubiquinol-cytochro
953	64	5.4	342	2	T11419	ubiquinol-cytochro
954	64	5.4	347	2	G01430	ubiquinol-cytochro
955	64	5.4	351	1	G01430	dopamine receptor
956	64	5.4	351	2	S56716	protein kinase SPK
957	64	5.4	367	1	T20271	PL6 protein - huma
958	64	5.4	369	1	H90587	hypothetical prote
959	64	5.4	376	1	S26031	hypothetical prote
960	64	5.4	376	2	G82656	ubiquinol-cytochro
961	64	5.4	378	2	D64181	ubiquinol-cytochro
962	64	5.4	379	1	GBBO	NA+/H+ antiporter
963	64	5.4	379	1	S17419	G protein-coupled
964	64	5.4	379	2	S26163	ubiquinol-cytochro
965	64	5.4	379	2	S43263	ubiquinol-cytochro
966	64	5.4	379	2	T11414	ubiquinol-cytochro
967	64	5.4	379	2	S58452	drug-efflux transp
968	64	5.4	383	2	S55594	probable na+/h+ an
969	64	5.4	383	2	S64667	hypothetical prote
970	64	5.4	383	2	H71848	acyltransferase [i
971	64	5.4	387	2	S74522	NADH2 dehydrogenas
972	64	5.4	387	2	AD1417	corticotropin-rele
973	64	5.4	402	2	A97559	branched-chain ami
974	64	5.4	402	2	AE2779	isocitrate dehydro
975	64	5.4	404	2	S26021	
976	64	5.4	404	2	A55610	
977	64	5.4	409	2	H81659	
978	64	5.4	422	2	E84338	

979	64	5.4	430	1	S32570	malC protein - Str
980	64	5.4	450	2	B40392	alpha-2-adrenergic
981	64	5.4	451	2	A36908	spore cortex penic
982	64	5.4	455	2	T31258	aromatic oxygenase
983	64	5.4	457	2	AF2975	aminotransferase,
984	64	5.4	457	2	B98307	hypothetical proce
985	64	5.4	463	2	AC0281	probable amino aci
986	64	5.4	469	2	H90322	polysaccharide bio
987	64	5.4	492	2	E58931	NADH2 dehydrogenas
988	64	5.4	503	2	JC7627	cytochrome P450 3A
989	64	5.4	511	2	T40334	hypothetical prote
990	64	5.4	527	2	A75122	sodium- and chlori
991	64	5.4	536	2	T36109	hypothetical prote
992	64	5.4	538	2	C90406	conserved hypothet
993	64	5.4	544	2	T13877	NADH2 dehydrogenas
994	64	5.4	562	2	T52481	cytochrome-c oxida
995	64	5.4	575	2	G75282	probable glutathio
996	64	5.4	586	1	A34400	ezrin [validated]
997	64	5.4	598	2	T05130	hypothetical prote
998	64	5.4	602	2	C75120	hypothetical prote
999	64	5.4	606	2	B69805	conserved hypothet
1000	64	5.4	608	2	G02640	polycystic kidney
1001	64	5.4	609	2	F70512	probable ATPase -
1002	64	5.4	610	2	S37049	H+-exporting ATPas
1003	64	5.4	614	2	A69845	Na+/H+ antiporter
1004	64	5.4	630	2	T41177	hypothetical prote
1005	64	5.4	654	2	C86677	DNA ligase (NAD) (
1006	64	5.4	657	2	T52460	hypothetical prote
1007	64	5.4	661	2	T51779	non-phototropic hy
1008	64	5.4	674	2	T50347	hypothetical prote
1009	64	5.4	696	2	AB1566	hypothetical prote
1010	64	5.4	748	2	T10651	hypothetical prote
1011	64	5.4	802	2	A87754	protein C43E11.11
1012	64	5.4	838	2	H82939	conserved hypothet
1013	64	5.4	860	2	T37768	probable vacuolar
1014	64	5.4	874	2	B86322	F6A14.8 protein -
1015	64	5.4	896	2	AF1409	the two components
1016	64	5.4	991	2	S57385	probable membrane
1017	64	5.4	1024	1	RNZQBF	DNA-directed RNA p
1018	64	5.4	1078	2	T19745	hypothetical prote
1019	64	5.4	1081	2	B81303	probable membrane
1020	64	5.4	1227	2	A33638	erythrocyte anion
1021	64	5.4	1385	2	T13415	hypothetical prote
1022	64	5.4	1462	1	DJHUAC	DNA-directed DNA p
1023	64	5.4	1695	2	JE0084	voltage-gated sodi
1024	64	5.4	2496	2	A71616	secreted protein P
1025	63.5	5.4	111	2	S43115	acidic ribosomal p
1026	63.5	5.4	123	2	G71692	NADH2 dehydrogenas
1027	63.5	5.4	147	2	AH0495	probable membrane
1028	63.5	5.4	149	2	H70581	hypothetical prote
1029	63.5	5.4	195	2	E71000	hypothetical prote
1030	63.5	5.4	214	2	C90191	conserved hypothet
1031	63.5	5.4	218	2	B71925	hypothetical prote
1032	63.5	5.4	218	2	T29205	cag island protein
1033	63.5	5.4	231	2	F85679	probable antirepre
1034	63.5	5.4	238	2	S75336	hypothetical prote
1035	63.5	5.4	241	2	F86691	ABC transporter pe
1036	63.5	5.4	242	1	S74794	hypothetical prote
1037	63.5	5.4	246	2	AD3574	brancheD-chain ami
1038	63.5	5.4	259	2	AF0106	probable membrane
1039	63.5	5.4	275	2	E95161	hypothetical prote
1040	63.5	5.4	275	2	D98027	hypothetical prote
1041	63.5	5.4	275	2	G84320	hypothetical prote
1042	63.5	5.4	276	2	E96951	conserved membrane
1043	63.5	5.4	280	2	T16240	hypothetical prote
1044	63.5	5.4	282	2	E83086	conserved hypothet
1045	63.5	5.4	282	2	AB0346	probable ABC trans
1046	63.5	5.4	291	2	AB2939	hypothetical prote
1047	63.5	5.4	291	2	E98343	hypothetical prote
1048	63.5	5.3	291	2	F75571	hypothetical prote
1049	63.5	5.3	313	2	D26696	NADH2 dehydrogenas
1050	63.5	5.3	315	2	E69365	hypothetical prote
1051	63.5	5.3	316	2	H86665	ferrichrome ABC tr

1052	63.5	5.3	327	2	S56162	MDCR15 protein - h
1053	63.5	5.3	328	2	D98215	oligopeptide ABC t
1054	63.5	5.3	328	2	T39824	septin homolog - f
1055	63.5	5.3	334	2	B72393	oligopeptide ABC t
1056	63.5	5.3	334	2	T41037	hypothetical prote
1057	63.5	5.3	334	2	T27081	hypothetical prote
1058	63.5	5.3	342	2	A38908	spa40 protein - Sh
1059	63.5	5.3	344	2	T34981	probable integral
1060	63.5	5.3	355	2	T15203	hypothetical prote
1061	63.5	5.3	359	2	D90172	hypothetical prote
1062	63.5	5.3	361	2	AE3071	hypothetical prote
1063	63.5	5.3	365	2	AB3494	oligopeptide trans
1064	63.5	5.3	372	2	S26667	G protein-coupled
1065	63.5	5.3	377	2	B72275	probable aspartate
1066	63.5	5.3	377	1	CBRT	probable aspartate
1067	63.5	5.3	381	2	T11312	ubiquinol-cytochro
1068	63.5	5.3	387	2	H88012	ubiquinol-cytochro
1069	63.5	5.3	389	2	G75133	protein K10B4.2 (i
1070	63.5	5.3	392	2	H71520	hypothetical prote
1071	63.5	5.3	395	2	B81358	probable hth trans
1072	63.5	5.3	398	2	C71682	transmembrane tran
1073	63.5	5.3	398	2	D81397	ubiquinol-cytochro
1074	63.5	5.3	399	2	B95080	cell division prot
1075	63.5	5.3	400	2	AG3016	phosphoglycerate k
1076	63.5	5.3	401	2	T46306	hypothetical prote
1077	63.5	5.3	404	1	LABECA	latent membrane pr
1078	63.5	5.3	406	2	T19887	hypothetical prote
1079	63.5	5.3	423	2	T04915	CDP-diacylglycerol
1080	63.5	5.3	423	2	G85255	CDP-diacylglycerol
1081	63.5	5.3	426	2	A96268	phosphoglycerate k
1082	63.5	5.3	426	2	T33299	hypothetical prote
1083	63.5	5.3	438	2	A82262	conserved hypothet
1084	63.5	5.3	444	2	B85789	hypothetical prote
1085	63.5	5.3	445	2	B81358	hypothetical prote
1086	63.5	5.3	445	2	T16025	hypothetical prote
1087	63.5	5.3	447	2	F90940	CDP-diacylglycerol
1088	63.5	5.3	447	2	S52437	CDP-diacylglycerol
1089	63.5	5.3	450	2	E96738	hypothetical prote
1090	63.5	5.3	452	2	T21118	hypothetical prote
1091	63.5	5.3	461	2	C97187	sugar transferase
1092	63.5	5.3	461	2	T48686	hypothetical prote
1093	63.5	5.3	468	2	H90562	mg2+ transport pro
1094	63.5	5.3	487	2	B95059	hypothetical prote
1095	63.5	5.3	491	2	A64939	hypothetical prote
1096	63.5	5.3	492	2	B90373	sugar transport re
1097	63.5	5.3	494	2	S76516	integral membrane
1098	63.5	5.3	494	2	T48385	transporter like p
1099	63.5	5.3	498	2	T16190	hypothetical prote
1100	63.5	5.3	500	2	AF2325	NADH dehydrogenase
1101	63.5	5.3	511	1	G90321	virulence factor m
1102	63.5	5.3	511	2	A70201	hypothetical prote
1103	63.5	5.3	525	2	A49601	nucleocapsid prote
1104	63.5	5.3	537	2	G82873	conserved hypothet
1105	63.5	5.3	540	1	A64454	uncharacterized me
1106	63.5	5.3	544	2	C96943	sterol O-acyltrans
1107	63.5	5.3	551	2	E64537	l-lactate permease
1108	63.5	5.3	551	2	D71969	probable peptide t
1109	63.5	5.3	555	2	G96744	probable L-lactate
1110	63.5	5.3	567	2	C75340	hyaluronoglucosami
1111	63.5	5.3	568	2	T17588	sodium/dicarboxyla
1112	63.5	5.3	593	2	I46528	protein ZK697.5 [i
1113	63.5	5.3	594	2	E88956	glucose transport
1114	63.5	5.3	605	2	A36361	glucose transport
1115	63.5	5.3	605	2	H71562	probable flagellar
1116	63.5	5.3	605	2	T43974	hypothetical prote
1117	63.5	5.3	610	2	T44161	hypothetical prote
1118	63.5	5.3	668	2	B54759	ba-type ubiquinol
1119	63.5	5.3	671	2	B37237	protein kinase C (
1120	63.5	5.3	681	2	AF0697	probable type III
1121	63.5	5.3	683	2	A85044	hypothetical prote
1122	63.5	5.3	708	2	JQ1148	killer toxin KHS p
1123	63.5	5.3	741	2	T20130	hypothetical prote
1124	63.5	5.3	780	2	T48189	probable transport
			787	2	A70132	cell division prot

ID			Len	N	Accession	Description
1125	63.5	5.3	819	2	T19351	hypothetical prote
1126	63.5	5.3	841	2	T38703	hypothetical prote
1127	63.5	5.3	843	2	T32487	hypothetical prote
1128	63.5	5.3	843	2	T41237	conserved hypothet
1129	63.5	5.3	844	2	AD2339	hypothetical prote
1130	63.5	5.3	951	2	T02376	probable cadmium-t
1131	63.5	5.3	966	2	T08987	hypothetical prote
1132	63.5	5.3	1004	2	H97717	hypothetical prote
1133	63.5	5.3	1098	2	G87323	hypothetical prote
1134	63.5	5.3	1229	2	S38100	SIP3 protein - yea
1135	63.5	5.3	1351	2	S42391	hypothetical prote
1136	63.5	5.3	1388	2	C71607	hypothetical prote
1137	63.5	5.3	1407	2	T17269	probable membrane
1138	63.5	5.3	1408	1	T00558	probable ABC trans
1139	63.5	5.3	1545	2	T47671	P-glycoprotein-lik
1140	63.5	5.3	1545	2	T42751	sulfonylurea recep
1141	63.5	5.3	1769	2	T46645	sulfonylurea recep
1142	63.5	5.3	2357	2	A59249	class VII unconven
1143	63.5	1	4725	1	A44357	dynein heavy chain
1144	63	1	96	1	WMVZP3	F3 protein - fowlp
1145	63	5.3	103	2	T20878	achaete-scute locu
1146	63	5.3	175	2	D70945	hypothetical prote
1147	63	5.3	230	2	H91224	Sec-independent pr
1148	63	5.3	230	2	B81705	maltose/maltodexri
1149	63	5.3	236	2	T17506	phosphoribosylamin
1150	63	5.3	249	2	F83520	geranylgeranyl tra
1151	63	5.3	257	2	T01891	cytochrome-c oxida
1152	63	5.3	258	2	S01165	sec-independent pr
1153	63	5.3	258	2	H65188	sec-independent pr
1154	63	5.3	280	2	F86071	sec-independent pr
1155	63	5.3	288	2	B87790	hypothetical prote
1156	63	5.3	290	2	B90013	probable permease
1157	63	5.3	301	2	A86743	probable permease
1158	63	5.3	306	2	H83620	hypothetical prote
1159	63	5.3	313	2	S65009	protein B0207.4 [i
1160	63	5.3	322	2	T29552	conserved hypothet
1161	63	5.3	329	2	C69804	NADH2 dehydrogenas
1162	63	5.3	332	2	A45211	hypothetical prote
1163	63	5.3	339	2	S56720	probable serine/th
1164	63	5.3	345	2	B83808	prostaglandin E re
1165	63	5.3	358	1	D84015	prostaglandin E re
1166	63	5.3	359	1	H91224	surface adhesion h
1167	63	5.3	361	2	T12364	hypothetical prote
1168	63	5.3	362	2	A42414	prostaglandin E re
1169	63	5.3	362	2	S65009	prostaglandin E re
1170	63	5.3	364	2	T29552	ubiquinol-cytochro
1171	63	5.3	365	2	S65009	ubiquinol-cytochro
1172	63	5.3	378	1	A42414	ubiquinol-cytochro
1173	63	5.3	379	1	S17412	ubiquinol-cytochro
1174	63	5.3	379	1	S17411	ubiquinol-cytochro
1175	63	5.3	379	1	S41833	ubiquinol-cytochro
1176	63	5.3	379	1	S41847	NADH2 dehydrogenas
1177	63	5.3	379	1	S43265	aspartate transami
1178	63	5.3	379	2	T11492	aromatic amino aci
1179	63	5.3	382	2	S58085	molybdopterin bios
1180	63	5.3	386	2	S58464	cell division prot
1181	63	5.3	389	2	S47882	proton/sodium-glut
1182	63	5.3	389	2	S60646	hypothetical prote
1183	63	5.3	391	2	H95003	arsenite transport
1184	63	5.3	396	2	C97876	corticotropin-rele
1185	63	5.3	398	2	D64541	cyclin 1a - maize
1186	63	5.3	405	2	E97947	hypothetical prote
1187	63	5.3	411	2	B70415	alpha-2A-adrenergi
1188	63	5.3	415	2	T20902	hypothetical prote
1189	63	5.3	420	2	G90154	NADH2 dehydrogenas
1190	63	5.3	431	2	S39535	hypothetical prote
1191	63	5.3	448	2	A57742	hypothetical prote
1192	63	5.3	450	2	T23809	hypothetical prote
1193	63	5.3	469	2	T30982	hypothetical prote
1194	63	5.3	475	2	A34169	hypothetical prote
1195	63	5.3	475	2	AE2188	hypothetical prote
1196	63	5.3	478	2	S52893	hypothetical prote
1197	63	5.3	478	2	C59095	hypothetical prote
1198	63	5.3	480	2	B70367	hypothetical prote
1199	63	5.3	481	2	S60260	stomatin-like prot
1200	63	5.3	490	2	C71541	probable na-depend
1201	63	5.3	491	2	AC1499	transmembrane prot
1202	63	5.3	493	2	T22376	hypothetical prote
1203	63	5.3	494	2	T14246	NADH2 dehydrogenas
1204	63	5.3	508	2	E90594	amino acid permeas
1205	63	5.3	509	1	A48508	membrane glycoprot
1206	63	5.3	527	2	T47744	probable nuclear d
1207	63	5.3	531	2	AH1491	hypothetical prote
1208	63	5.3	533	2	T47744	flagellar basal-bo
1209	63	5.3	534	2	A93316	protein Similar to
1210	63	5.3	535	2	AF1835	hypothetical prote
1211	63	5.3	562	2	B70081	hypothetical prote
1212	63	5.3	565	2	B86359	probable membrane-
1213	63	5.3	565	2	C70136	two-component sens
1214	63	5.3	569	2	T06153	probable membrane
1215	63	5.3	579	2	T47566	two-component sens
1216	63	5.3	583	2	T26574	ABC transporter AT
1217	63	5.3	584	2	F95910	hypothetical prote
1218	63	5.3	598	2	G99789	replication licens
1219	63	5.3	600	2	B83875	hypothetical prote
1220	63	5.3	608	2	S66954	NADH2 dehydrogenas
1221	63	5.3	677	2	AD2000	NADH2 dehydrogenas
1222	63	5.3	677	2	G84829	NADH2 dehydrogenas
1223	63	5.3	682	1	F95910	protein H26D21.2 [
1224	63	5.3	701	2	T13568	NADH2 dehydrogenas
1225	63	5.3	702	2	H64485	probable sugar tra
1226	63	5.3	704	2	T12677	proton pump, proba
1227	63	5.3	712	2	T13665	NADH2 dehydrogenas
1228	63	5.3	729	2	D87418	S-protein secretio
1229	63	5.3	737	2	T06127	proton pump, proba
1230	63	5.3	738	2	139547	probable sugar tra
1231	63	5.3	769	2	S58612	NADH2 dehydrogenas
1232	63	5.3	813	2	C87740	hypothetical prote
1233	63	5.3	849	1	S49844	voltage-dependent
1234	63	5.3	869	2	B45082	voltage-dependent
1235	63	5.3	943	2	T17297	putative sodium ch
1236	63	5.3	960	2	T12677	protein H26D21.2 [
1237	63	5.3	1030	2	A42497	neurotrophic recep
1238	63	5.3	1034	2	B86880	hypothetical prote
1239	63	5.3	1082	2	H70360	anion exchanger 3,
1240	63	5.3	1212	2	B82809	SWI/SNF family hel
1241	63	5.3	1227	2	B34911	cation efflux syst
1242	63	5.3	1532	2	T18438	exodeoxyribonuclea
1243	63	5.3	1646	2	JH0422	band 3-related pro
1244	63	5.3	1854	2	T39035	hypothetical prote
1245	63	5.3	2203	2	T42742	DNA-damage-inducib
1246	63	5.3	2295	2	T22698	type III secretion
1247	63	5.3	4488	1	RRIHM2	genome polyprotein
1248	62.5	5.3	107	2	A42497	hypothetical prote
1249	62.5	5.2	140	2	B69262	hypothetical prote
1250	62.5	5.2	168	2	B88739	hypothetical prote
1251	62.5	5.2	168	2	B83851	hypothetical prote
1252	62.5	5.2	173	2	JC1169	hypothetical prote
1253	62.5	5.2	178	2	D71702	hypothetical prote
1254	62.5	5.2	181	2	S67379	hypothetical prote
1255	62.5	5.2	200	2	G82911	hypothetical prote
1256	62.5	5.2	232	2	A71895	hypothetical prote
1257	62.5	5.2	236	2	T22698	hypothetical prote
1258	62.5	5.2	240	2	F83705	hypothetical prote
1259	62.5	5.2	245	2	H70091	hypothetical prote
1260	62.5	5.2	245	2	T20810	potassium channel
1261	62.5	5.2	258	2	S10658	hypothetical prote
1262	62.5	5.2	258	2	B91201	hypothetical prote
1263	62.5	5.2	274	2	A86048	type III secretion
1264	62.5	5.2	274	2	AC2946	escT [imported] -
1265	62.5	5.2	274	2	G98336	hypothetical prote
1266	62.5	5.2	276	2	G72292	sorbitol/mannitol
1267	62.5	5.2	276	2	H83568	glycerol-3-phospha
1268	62.5	5.2	280	2	T24579	probable permease
1269	62.5	5.2	289	2	T11063	NADH2 dehydrogenas
1270	62.5	5.2	293	2	D82504	hypothetical prote
					AH0075	probable permease

ID			Num	Ct	Code	Description
1271	62.5	5.2	296	2	H83480	cytochrome o ubiqu
1272	62.5	5.2	298	2	T37251	homeobox protein c
1273	62.5	5.2	299	2	T26365	hypothetical prote
1274	62.5	5.2	326	2	C90272	hypothetical prote
1275	62.5	5.2	333	2	AB1925	hypothetical prote
1276	62.5	5.2	333	2	A81925	hypothetical prote
1277	62.5	5.2	333	2	B89010	protein R08F11.2	
1278	62.5	5.2	335	2	T41426	hypothetical prote
1279	62.5	5.2	349	2	H95060	ABC transporter, p
1280	62.5	5.2	349	2	D97929	probable integral
1281	62.5	5.2	352	2	E81450	probable integral
1282	62.5	5.2	358	2	E83829	hypothetical prote
1283	62.5	5.2	365	2	F82210	amino acid ABC tra
1284	62.5	5.2	369	2	C88030	protein F46F5.10	
1285	62.5	5.2	370	2	C69309	conserved hypothet
1286	62.5	5.2	379	1	S17407	ubiquinol-cytochro
1287	62.5	5.2	379	2	S58462	ubiquinol-cytochro
1288	62.5	5.2	379	2	S58057	conserved hypothet
1289	62.5	5.2	382	1	A44227	omega-3 fatty acid
1290	62.5	5.2	383	2	A72373	conserved hypothet
1291	62.5	5.2	383	2	F84771	hypothetical prote
1292	62.5	5.2	388	2	T31738	Na+/H+-exchanging
1293	62.5	5.2	391	2	C64722	aromatic amino aci
1294	62.5	5.2	399	2	A86632	hypothetical prote
1295	62.5	5.2	404	2	H83249	sodium/glutamate s
1296	62.5	5.2	405	1	QBE35	BBRF3 protein - hu
1297	62.5	5.2	406	2	H89006	protein T22F3.11	
1298	62.5	5.2	409	2	C89942	conserved hypothet
1299	62.5	5.2	413	2	AC1369	multidrug resistan
1300	62.5	5.2	417	2	T51467	glucose 6 phosphat
1301	62.5	5.2	420	2	D95018	conserved hypothet
1302	62.5	5.2	420	2	E97891	conserved hypothet
1303	62.5	5.2	422	2	C70518	probable nanT prot
1304	62.5	5.2	425	2	E97172	flagellin [importe
1305	62.5	5.2	426	2	F30010	ct266 hypothetical
1306	62.5	5.2	426	2	E86542	CT266 hypothetical
1307	62.5	5.2	431	2	H84069	hypothetical prote
1308	62.5	5.2	440	2	T20092	hypothetical prote
1309	62.5	5.2	442	1	JQ1042	endothelin recepto
1310	62.5	5.2	443	2	F30010	NADH2 dehydrogenas
1311	62.5	5.2	443	2	T08136	probable omega-6 d
1312	62.5	5.2	452	2	G64844	probable membrane
1313	62.5	5.2	452	2	G85647	hypothetical prote
1314	62.5	5.2	455	2	G90787	hypothetical prote
1315	62.5	5.2	457	2	D97217	glycosyltransferas
1316	62.5	5.2	457	2	F69662	UDP-N-acetylmuramo
1317	62.5	5.2	459	2	AF3284	high-affinity bran
1318	62.5	5.2	461	2	S57713	probable mannosyl
1319	62.5	5.2	468	2	A49131	inositol 1,4,5-tri
1320	62.5	5.2	470	2	C70641	hypothetical prote
1321	62.5	5.2	487	2	S73161	hypothetical prote
1322	62.5	5.2	490	2	T40116	hypothetical prote
1323	62.5	5.2	492	2	AC0768	probable transmemb
1324	62.5	5.2	494	2	AC0768	hypothetical prote
1325	62.5	5.2	501	1	T15502	head protein gp5 -
1326	62.5	5.2	502	2	JN0539	hypothetical prote
1327	62.5	5.2	505	2	C86263	f42h10.1 protein -
1328	62.5	5.2	507	2	S44647	probable membrane
1329	62.5	5.2	546	2	S52677	probable membrane
1330	62.5	5.2	547	2	AE0571	probable membrane
1331	62.5	5.2	568	2	S64567	hypothetical prote
1332	62.5	5.2	569	2	S64332	NADH2 dehydrogenas
1333	62.5	5.2	572	2	T22928	interleukin-10 rec
1334	62.5	5.2	578	2	T11478	hypothetical prote
1335	62.5	5.2	580	2	T11451	NADH2 dehydrogenas
1336	62.5	5.2	601	2	T02596	hypothetical prote
1337	62.5	5.2	608	2	T34391	myosin-light-chain
1338	62.5	5.2	610	2	A28798	probable cellulose
1339	62.5	5.2	621	2	B95897	white homolog - hu
1340	62.5	5.2	638	2	G02068	intensifier 1 prot
1341	62.5	5.2	668	2	C71868	hypothetical prote
1342	62.5	5.2	685	2	T04073	hypothetical prote
1343	62.5	5.2	697	2	T19254	hypothetical prote

ID			Num	Ct	Code	Description
1344	62.5	5.2	704	2	S46000	probable membrane
1345	62.5	5.2	718	2	T05840	subtilisin-like pr
1346	62.5	5.2	763	2	T27937	hypothetical prote
1347	62.5	5.2	807	2	T28279	ORF MSV119 probabl
1348	62.5	5.2	815	2	G97266	mannose-1-phosphat
1349	62.5	5.2	837	2	D71027	hypothetical prote
1350	62.5	5.2	848	2	A33810	band 3 anion trans
1351	62.5	5.2	865	2	G96574	probable membrane
1352	62.5	5.2	881	2	H71719	probable membrane
1353	62.5	5.2	971	2	T41988	hypothetical prote
1354	62.5	5.2	1082	2	A81983	probable DNA-direc
1355	62.5	5.2	1144	2	C87691	hypothetical prote
1356	62.5	5.2	1195	2	T17242	hypothetical prote
1357	62.5	5.2	1291	2	T20642	hypothetical prote
1358	62.5	5.2	1291	2	B87998	protein F09C3.1 [li
1359	62.5	5.2	1397	2	T17172	hypothetical prote
1360	62.5	5.2	1576	2	E71410	protein F37C4.1 [li
1361	62.5	5.2	1676	2	T43144	vitellogenin II pr
1362	62.5	5.2	1687	2	T43963	probable centromer
1363	62.5	5.2	1951	2	S13553	RNA viral polymera
1364	62.5	5.2	2150	2	T11073	hypothetical prote
1365	62	5.2	112	2	D82954	NADH2 dehydrogenas
1366	62	5.2	132	2	E84028	hypothetical prote
1367	62	5.2	174	2	IMECB	cell-shape determi
1368	62	5.2	175	1	E97217	colicin B immunity
1369	62	5.2	198	2	G90134	uncharacterized co
1370	62	5.2	201	2	P89840	hypothetical prote
1371	62	5.2	206	2	A88056	conserved hypothet
1372	62	5.2	209	2	T32573	probable sugar ABC
1373	62	5.2	225	2	B65127	hypothetical prote
1374	62	5.2	247	1	P75433	hypothetical prote
1375	62	5.2	273	2	AC1332	probable permease
1376	62	5.2	285	2	E70010	probable sugar upt
1377	62	5.2	287	2	H95943	cytochrome-c oxida
1378	62	5.2	298	2	A10209	cytochrome-c oxida
1379	62	5.2	305	2	A69838	conserved hypothet
1380	62	5.2	306	2	S36953	interleukin-8 rece
1381	62	5.2	312	2	S83356	hypothetical prote
1382	62	5.2	315	2	T29189	hypothetical prote
1383	62	5.2	331	2	T43972	chalcone reductase
1384	62	5.2	345	2	T24821	chalcone reductase
1385	62	5.2	351	2	S48851	hypothetical prote
1386	62	5.2	351	2	S48849	hypothetical prote
1387	62	5.2	353	2	T24821	hypothetical prote
1388	62	5.2	360	2	AB3117	hypothetical prote
1389	62	5.2	362	2	AB3117	F3H9.12 protein -
1390	62	5.2	363	2	T05987	hypothetical prote
1391	62	5.2	370	2	T32203	response regulator
1392	62	5.2	377	2	B82954	response regulator
1393	62	5.2	377	2	C86408	hypothetical prote
1394	62	5.2	379	2	C98170	hypothetical prote
1395	62	5.2	381	2	A53611	interleukin-8 rece
1396	62	5.2	383	2	T33260	translocation prot
1397	62	5.2	398	1	B57641	ubiquinol-cytochro
1398	62	5.2	399	2	S42379	ubiquinol-cytochro
1399	62	5.2	399	2	H84111	hypothetical prote
1400	62	5.2	377	2	T05427	bicyclomycin resis
1401	62	5.2	379	2	T05427	conserved hypothet
1402	62	5.2	381	2	E58851	cell-division prot
1403	62	5.2	383	1	E58851	xylose operon regu
1404	62	5.2	381	2	T11440	conserved hypothet
1405	62	5.2	398	1	C95965	cbs domain protein
1406	62	5.2	399	2	E64112	protein-tyrosine-p
1407	62	5.2	399	2	F72417	protein-tyrosine-P
1408	62	5.2	400	2	JC5279	hypothetical prote
1409	62	5.2	402	2	AB1565	hypothetical prote
1410	62	5.2	402	2	D70186	probable transmemb
1411	62	5.2	411	2	H72084	hypothetical prote
1412	62	5.2	432	1	A34845	hypothetical prote
1413	62	5.2	432	2	T21880	hypothetical prote
1414	62	5.2	432	2	T47737	hypothetical prote
1415	62	5.2	444	2	F81367	probable transmemb
1416	62	5.2	454	2	H65054	hypothetical prote

ID					Accession	Description
1417	62	5.2	458	2	A84487	probable replicati
1418	62	5.2	466	2	AH1800	transmembrane effl
1419	62	5.2	474	2	E64232	hypothetical prote
1420	62	5.2	483	2	S46124	nuclear protein EN
1421	62	5.2	487	2	T05271	probable 3-oxoacyl
1422	62	5.2	497	1	T20799	hypothetical prote
1423	62	5.2	497	2	S53834	NADH2 dehydrogenas
1424	62	5.2	499	2	S66834	probable membrane
1425	62	5.2	502	2	B81914	probable periplasm
1426	62	5.2	514	2	AE23372	hypothetical prote
1427	62	5.2	528	1	A96671	Ammonium transport
1428	62	5.2	555	2	ACCH2N	nicotinic acetylch
1429	62	5.2	567	2	T08869	protein P2 - Acyrt
1430	62	5.2	582	2	S29498	lymphocyte antigen
1431	62	5.2	585	2	S19424	hypothetical prote
1432	62	5.2	600	2	T02360	hypothetical prote
1433	62	5.2	600	2	H98149	ATP-binding transp
1434	62	5.2	630	2	AD3138	hypothetical prote
1435	62	5.2	644	2	H83686	PTS system, beta-g
1436	62	5.2	660	2	T20034	hypothetical prote
1437	62	5.2	667	2	A44432	amino acid transpo
1438	62	5.2	675	1	S46952	hypothetical prote
1439	62	5.2	675	2	T20822	phosphotransferase
1440	62	5.2	678	2	F71921	hypothetical prote
1441	62	5.2	702	2	T03903	hypothetical prote
1442	62	5.2	707	2	A35804	nucleolin - human
1443	62	5.2	707	2	T25030	heat shock protein
1444	62	5.2	724	1	A29232	hypothetical prote
1445	62	5.2	739	2	S73829	101K malaria antig
1446	62	5.2	743	2	A88679	probable ABC trans
1447	62	5.2	750	2	A46616	protein H06H21.10
1448	62	5.2	756	1	A33380	cytochrome-c oxida
1449	62	5.2	791	2	T09455	interleukin-4 rece
1450	62	5.2	810	1	E95092	vacuolar assembly
1451	62	5.2	841	2	T42556	aminopeptidase N	
1452	62	5.2	848	2	TNBEEH	tegument protein 1
1453	62	5.2	864	1	S70958	97K alpha trans-in
1454	62	5.2	872	2	C70191	otnA protein - Vib
1455	62	5.2	911	2	PWBYR1	penicillin-binding
1456	62	5.2	932	1	G97217	Ca2+-transporting
1457	62	5.2	950	2	AE3557	conserved membrane
1458	62	5.2	1002	2	T13163	acriflavin resista
1459	62	5.2	1024	2	T43458	Rab6 GTPase activa
1460	62	5.2	1030	2	T29010	hypothetical prote
1461	62	5.2	1031	2	G88480	hypothetical prote
1462	62	5.2	1041	2	C96767	protein C16A3.7 [i
1463	62	5.2	1273	2	T18939	unknown protein F2
1464	62	5.2	1283	2	A60165	hypothetical prote
1465	62	5.2	1321	2	T20695	sodium channel pro
1466	62	5.2	1780	2	T33783	hypothetical prote
1467	62	5.2	1802	2	T31679	bacitracin synthet
1468	62	5.2	6359	2	B99233	hypothetical prote
1469	62		99	2	E69985	hypothetical prote
1470	62		134	2	C86655	hypothetical prote
1471	62		149	2	S43955	hypothetical prote
1472	62		150	2	S77185	probable NADH2 deh
1473	61.5	5.1	159	2	AF2618	hypothetical prote
1474	61.5	5.1	162	2	E97400	lipoprotein signal
1475	61.5	5.1	162	2	JC5045	epithelial membran
1476	61.5	5.1	163	2	H97775	hypothetical prote
1477	61.5	5.1	173	2	G89947	hypothetical prote
1478	61.5	5.1	176	2	S40726	hypothetical prote
1479	61.5	5.1	183	2	H70478	hypothetical prote
1480	61.5	5.1	185	2	H69327	conserved hypothet
1481	61.5	5.1	190	2	A26630	nucleoplasmin A -
1482	61.5	5.1	212	2	A83521	hypothetical prote
1483	61.5	5.1	225	2	T19811	conserved hypothet
1484	61.5	5.1	264	2	T18998	conserved hypothet
1485	61.5	5.1	272	2	G82888	hypothetical prote
1486	61.5	5.1	273	2	T28980	hypothetical prote
1487	61.5	5.1	274	2	S42168	NADH2 dehydrogenas
1488	61.5	5.1	276	2	F72342	conserved hypothet
1490	61.5	5.1	278	2	D83080	hypothetical prote
1491	61.5	5.1	279	2	AG0421	sugar transport sy
1492	61.5	5.1	284	2	AC3429	perosamine synthet
1493	61.5	5.1	289	2	F91269	hypothetical prote
1494	61.5	5.1	289	2	D86110	hypothetical prote
1495	61.5	5.1	290	2	AE0947	ribonuclease BN (E
1496	61.5	5.1	292	2	AE1539	sugar ABC transpor
1497	61.5	5.1	293	2	C90032	hypothetical prote
1498	61.5	5.1	293	2	A83710	ABC transporter (p
1499	61.5	5.1	293	2	B69866	transcription regu
1500	61.5	5.1	294	2	AD0886	probable oxidoredu

ALIGNMENTS

RESULT 1
I38027
MLN 64 protein - human
C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: I38027; S60682
R;Tomasetto, C.; Regnier, C.H.; Moog-Lutz, C.; Mattei, M.G.; Chenard, M.P.; Lidereau, R.
Genomics 28, 367-376, 1995
A;Title: Identification of four novel human genes amplified and overexpressed in breast
A;Reference number: I37080; MUID:96039245; PMID:7490069
A;Accession: I38027
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-445 <RES>
A;Cross-references: UNIPROT:Q14849; UNIPARC:UPI000012F1BC; EMBL:X80198; NID:g951278; PID
C;Genetics:
A;Gene: MLN64

Query Match 55.6%; Score 664; DB 2; Length 445;
Best Local Similarity 56.2%; Pred. No. 8.7e-55;
Matches 135; Conservative 38; Mismatches 45; Indels 22; Gaps 5;

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Qy   1 MNHLP-----EDMENALL-----TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDV  51
               |     ||  ||       :|| : || | |  ::| | |:   || :: ||   ||:
Db   1 MSKLPRELTRDLERSLPAVASLGSSLSHSQSLSSHHLPPPE-----KRRAISDV  49

Qy  52 RRTFCLFVTFDLLFVTLLWIIELNVNGGIENTLEKEVWQYDYSSSYFDIFLLAVFRFKVL 111
        |||||||||||||  :|||||||| || | |: : :  ||:|: || | ||| ||||
Db  50 RRTFCLFVTFDLLFISILWIIELNTNTGIRKNLEQEIIQYNFKTSFFDIFVLAFFRFSGL 109

Qy 112 ILAYAVCRLRHWAIALITTAVTSAFLLAKVTLSKLFSQGAPGYVLPIISFILAWIETWFL 171
        :||||| |||| |:| ||:||| |||  |:|:|:|:: |: : || :|:|||| |||| |
Db 110 LLGYAVLQLRHWVIAVTTLVSSAFLIVKVTLSELLSKGAPGYLLPIVSFVLAWLETWFL 169

Qy 172 DFKVLPQEAEEENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSE-EAEEKQDSEK 229
        ||:|||||| ||:||  ||:  |:| || | ::|  |||||||: |:|| |: |:  :||
Db 170 DFKVLPQEAEERWYLAAQVAVARGPLLFSCALSEGQFYSPPESFAGSDNESDEEVAGKK 229
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RESULT 2
T16170
hypothetical protein F26F4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16170
R;Fulton, L.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid F26F4.
A;Reference number: Z18471
A;Accession: T16170
A;Molecule type: DNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-478 <FUL>
A;Cross-references: UNIPROT:Q19819; UNIPARC:UPI00017B938; EMBL:U12964; NID:g1213452; PI
C;Genetics:
A;Experimental source: strain Bristol N2

RESULT 3

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A;Gene: CESP:F26F4.4
A;Introns: 47/2; 81/2; 125/3; 171/3; 214/1; 236/2; 343/3; 444/1

Query Match          17.1%;    Score 204;  DB 2;   Length 478;
Best Local Similarity  26.5%;  Pred. No. 2.5e-11;
Matches  56;   Conservative  36;   Mismatches  73;   Indels  46;   Gaps  6;

Qy     42  GREKKGISDVRRTFCLFVTFDLLFVTLLWII---------------ELNVNGGIENTLEK 86
               ||:| | :: |  |||| ||                         :|| ||| ||
Db     69  GSQRIGVSKDRKRFIVITFPDTSITILLWLLCTVTRDDDWDKVFFNEINI------FNP 121

Qy     87  EVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAITTAVTSAFLLAKVILSKL 146
               | ||| ::: |||||||||||| ||||||||||||||||||  ||| |||||:|||
Db    122  KFIRI-----SLFDIVLLAVRLMLLIGVVVGICLLVKQWYTVAFTTLASSAYILMKVLFYEN 177

Qy    147  FSQGAFGYVLPII-SFILAWIETWFLDFKVLPQEAEEENRLLIVQDASERAALIPGGLSD 205
               |||||||||||| |||| ||||||||||||||||||||| ||||||
Db    178  HSSSAVPLLLIITSFTLCWSEFYLMPFQILPRERYARREL------------DGIEN 224

Qy    206  GQFYSPPESEA---------GSEEAEEKODSEKP 230
               |     ||
Db    225  PEFSTDDEARSNNRHRGRQQNSGNQSEAP 255
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A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: H90281
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-348  <KUR>
A;Cross-references: UNIPARC:UPI0000064305; GB:AE006641; NID:g13814471; 
A;Genetics:
A;Gene: dppB-1
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hypothetical protein dppB-1 [imported] - Sulfolobus solfataricus

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C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
```

R.She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001

RESULT 4

D75080

glucose-1-phosphate thymidylyltransferase related protein PAB2433 - Pyrococcus abyssi

```
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
R;anonymous, Genoscope
C;Accession: D75080
submitted to the EMBL Data Library, July 1999
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A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: D75080
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-424  <KAW>
A;Cross-references: UNIPROT:Q9UZW1; UNIPARC:UPI0000034071C; GB:AJ248286; GB:AL096836; NID
A;Experimental source: strain Orsay
A;Genetics:
A;Gene: PAB2433
C;Superfamily: Aquifex aeolicus glucose-1-phosphate thymidylyltransferase
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Query Match           7.8%;    Score 93.5;  DB 2;   Length 424;
Best Local Similarity  21.9%;  Pred. No. 0.57;
Matches  47;   Conservative  25;   Mismatches  72;   Indels  71;   Gaps  7;

Qy      5  PEDMENA------------------------LTGSQSSHASLRNIHSINPTQLMARIESYEGRE 44
              |||||                         |||||||||||||||||||||
Db    207  PEDIKKARKLIVTISVKGVGDGFISRHLNRKISTRISALLVEHVTPNQM----------- 255

Qy     45  KKGISDVRRTFCLFVTFDL--LFVTLLWIIELNVNG----------GIENTLEKEWQYDY 93
              |||||||||||     |||  ||| | |          |  ||||| ||| |
Db    256  ----------TIVTFLFGIFSALMNFISVPIAGILYQVSSILDGVDGEIARARMQTSK 303

Qy     94  YSSYFDIFLLAVFRFK-VLILAYAVCRLRHWWAIAITTAVTSAFL-------------L 138
               ::|||||||||:|  |||||::|  ||||| |
Db    304  FGGYFDSILDRYVDTFLLILAVSIREPLWWAIAIAIAMFSSAMYSYSTERFKGAYCVDA 363

Qy    139  AKVI--LSKLFSQGAFGYVLPIISFILAWIETWFL 171
              ||||  |: | ||| | |||||||  :|||||||
Db    364  YKVIPALRKVPGKDERIFLTMLLTLVGWIKALFL 398
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RESULT 5

T43048

calcium channel alpha-1 chain - Cyanea capillata

```
C;Species: Cyanea capillata
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43048
```

R;Jeziorski, M.C.; Greenberg, R.M.; Clark, K.S.; Anderson, P.A.V.
J. Biol. Chem. 273, 22792-22799, 1998
A;Title: Cloning and functional expression of a voltage-gated calcium channel alphal sub

```
A;Reference number: Z22300; MUID:98380510; PMID:9712913
A;Accession: T43048
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1911  <JEZ>
A;Cross-references: UNIPROT:O02038; UNIPARC:UPI000007C488; EMBL:U93075; NID:g1947095; PI
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: transmembrane protein
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Query Match           7.5%;    Score 90;  DB 2;   Length 1911;
Best Local Similarity  23.5%;  Pred. No. 7.2;
Matches  43;   Conservative  33;   Mismatches  59;   Indels  48;   Gaps  9;

Qy      5  PEDMENALTGSQSSHASLRNIHSINPTQLM-----ARIESYEGREKKGISDV 51
              ||| ||      |||||||||||||||||||
Db    791  PEDVE--LGNPKSKNGTLRHMGETTSTEMSEGKEARIRPLRLSELNLLKDIPDPMPPESS 848

Qy     52  -------RRTFCLFVTFDLLFVT--LLMIIELNVNGGIENTLEKEVMQYDYYSSYFDI 100
                      |||| ||||| |    ::|| ||  :||||||||||
Db    849  FFIFSANNKLRYLCYRLAVNKIFINSILVLIIMSSVALAAEDPIGRDVLR-NKILGYFDI 907

Qy    101  FLLAVFRFKVLI--LAYAV---------CR---------LRHWWAIAITT-AVTSAFLLA 139
              |||||||||:|  :|||:         ||         ||||| ||||  |||||||||
Db    908  FPTAMPTFEVTVKMIAFGVILHKRSFCRSFFNQLDLVIVAVSWAAIMLSRGSATSVVRIL 967

Qy    140  KVI 142
              |:|
Db    968  RVL 970
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RESULT 6

T21969
hypothetical protein F38E11.7 - Caenorhabditis elegans
R;Matthews, P.
submitted to the EMBL Data Library, January 1996
C;Species: Caenorhabditis elegans
A;Reference number: Z19495
A;Accession: T21969
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-767 <WIL>
A;Cross-references: UNIPROT:Q20170; UNIPARC:UPI00000074B2B; EMBL:Z68342; PIDN:CAA92775.1;
.;E.M.; de Vos, N.; van Ommen, G.J.B.; Breuning, M.H.; Doggett, N.A.; Meincke, L.J.; Liu,
C;Experimental source: clone F38E11
C;Genetics:
A;Gene: CESP:F38E11.7
A;Map position: 4
A;Introns: 50/2; 118/1; 139/2; 189/3; 226/1; 248/1; 287/2; 375/2; 432/3; 465/3; 548/1; 6

Best Local Similarity   24.8%;   Score 86.5; DB 2; Length 767;
Matches 35; Conservative 22; Mismatches 49; Indels 35; Gaps   5;

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Qy  61 FDLLFVTLLWIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVPRFKVLIL--AYAV 117
          |::||  |::|  |:|: |:||::|:|||:::||::||||| |||:|     ||:|
Db 109 FDILLRSMLSFYE---DGVLITSFSETWRHYVHSFYFAIDLLAIFPFDVLLIRKTSAAF 164

Qy 118 CRLRHWW-----------AIALTTAVTSAFLLAKVILSKLFSQGAFGVVLPI 158
        |:||          |:|::::::||::|||||:|||:|||::|  ||
Db 165 CRLNRFLKIYRIANFIAQSYGKLTQVTISLSKIFTACFLLFHV----NACVFYIISV 217

Qy 159 ISFILAW--IETWFLDFKVLP 177
        ||::|    ::|:|::|||:|
Db 218 NSDTSSWDGVNATFDDDEYLP 238
```

Qy 157 PIISFILAWIETWFLDFKVLPQ-EAEEENRLLIVQDASERAALI 199
Db 334 PYLEFVACNIE--FKNGRILANLEGKKEGSSAIINNLNNKAALM 375

RESULT 7
B81299
probable molybdopterin biosynthesis protein Cj1519 [imported] - Campylobacter jejuni (st
C;Species: Campylobacter jejuni
A;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
A;Accession: B81299
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: B81299
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-396 <PAR>
C;Genetics:
A;Gene: moeA2; Cj1519
A;Superfamily: molybdenum cofactor molybdenum incorporation protein MoeA
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

Best Local Similarity   21.0%;   Score 85.5; DB 2; Length 396;
Matches 47; Conservative 35; Mismatches 81; Indels 61; Gaps   9;

```
Qy   4 LPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLF----- 58
          |:|    ::|:|      ::|
Db 185 LGEALENPAQIRSSNHIAIANL---------------AKNLNCDRVFPLLKDDEK 225

Qy  59 VTFDLLFVTLLWIELNVNGGIE---NTLEKEVMQYDYSSYFDI----------- 100
Db 226 AFFSTLESALQSCDILVTTGGVSMGDFDFLKKAIKEYEIIIDKADIKPGRHIKIAKANEK 285

Qy 101 FLLAV--FRFKVLLLAYAVCR--LRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGVYL 156
Db 286 FIIALPGFFYSAMVMFNLYTRELINSW-----------------LLQPKDYICKAFLQSSYKKKT 333
```

RESULT 8
A57219
Batten disease-related protein CLN3 - human
C;Species: Homo sapiens (man)
A;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004
A;Accession: A57219
R;Lerner, T.J.; Boustany, R.M.N.; Anderson, J.W.; D'Arigo, K.L.; Schlumpf, K.; Buckler,
Cell 82, 949-957, 1995
A;Reference number: A57219; MUID:96016090; PMID:7553855
A;Accession: A57219
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Map position: 16p12.1-16p11.2
A;Residues: 1-438 <LER>
A;Cross-references: UNIPROT:Q13286; UNIPARC:UPI0000000ED; GB:U32680; NID:g1039422; PIDN
C;Genetics:
A;Gene: GDB:CLN3
A;Cross-references: GDB:120593; OMIM:204200
A;Superfamily: CLN3 protein/Battenin (Batten disease protein)
C;Keywords: membrane protein
A;Title: Isolation of a novel gene underlying Batten disease, CLN3.

Best Local Similarity   25.5%;   Score 85.5; DB 2; Length 438;
Matches 38; Conservative 18; Mismatches 46; Indels 47; Gaps   8;

```
Qy  64 LFVTLLWII--------------ELNVNGGI------ENTLEKEVMQYDYSSYFDIFLLAVPRF 108
Db 277 VFKGLLWYIVPLVVYFAEYFINQGLFELLFFWNTSLSHAQQYRWYQM---LYQAGVFAS 333

Qy 109 KVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGVYLPIISFIL----- 163
Db 334 R--SSLRCCRIRFTWALALLQCLNLVFLLADV-----------------WFGF-LPSIYLVFLILY 380

Qy 164 ------AWIETWFLDFKVLPQEAEEENR 185
Db 381 EGLLGGAAYVNT----FHNIALETSDEHR 405
```

RESULT 9
G70172
conserved hypothetical integral membrane protein BB0584 - Lyme disease spirochaete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
A;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
A;Accession: G70172
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: G70172
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-448 <KLE>
A;Cross-references: UNIPROT:O51531; UNIPARC:UPI0000005752F; GB:AE001160; GB:AE000783; NID
A;Experimental source: strain B31
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.

Best Local Similarity   24.4%;   Score 85; DB 2; Length 448;
Matches 47; Conservative 28; Mismatches 64; Indels 54; Gaps 11;

```
Qy  50 DVRRTFCLFVTFDLLFVTL---IWIIELNVNGGIE-NTLEKEVMQYDYSS------Y 97
Db 271 DTHKYAAYSISFSIYFIIFNIIHSPCISLNIMGYEMHNSKKEIMKVAIYLSKIGLKLAF 330
```

```
Qy    98  FDIFLLAVFRFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVI--LSKLFSQGA---- 151
              ||| ||::       : |:  |:|: | : : : |:|
Db   331  LTSFVLFIFSFFAPVIFYL-KYSHLIGILIRYSSVSAFFMALAFQYLFGFFRAGASPSF 389

Qy   152  -----FGYVLPIISFILAWIETWFFLDFKVLPQEAEEENRLLIV------QDASERAA 197
               :|||| |: ::| : ||: :  |:          :|:  ::
Db   390  GAIMEGSVTFVYTIP-IAFVLA------NYTNLPFE------IIVFIPSLEDAIKLVV 434

Qy   198  LIPCGLSDGQFYS 210
              :|       ||:
Db   435  SLP------YFYS 441
```

RESULT 10

A41680

integral membrane protein pssA - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Jun-1992
A;Accession: A41680
R;Kuge, O.; Nishijima, M.; Akamatsu, Y.;
J. Biol. Chem. 266, 24184-24189, 1991
A;Title: A Chinese hamster cDNA encoding a protein essential for phosphatidylserine synt
A;Reference number: A41680; MUID:92084729; PMID:1748687
A;Accession: A41680
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-471 <KUG>
A;Cross-references: UNIPARC:UPI000012280F; GB:D10234; GB:D90468; NID:g220280; PIDN:BAA01
C;Superfamily: membrane protein
C;Keywords: membrane protein

```
Query Match             7.1%;   Score 84.5;   DB 2;   Length 471;
Best Local Similarity  24.4%;   Pred. No. 4.6;
Matches  32;   Conservative  22;   Mismatches  38;   Indels  39;   Gaps  7;

Qy    55  FCLFVTFDLLFVTLLIWIIELNVNGGIENTLEKEVMQY-----------DYYSSYFDIFLLAV 105
              | |  :|| |: :::            | |      :          :||||||| |:
Db   117  FLLFLNFEQVKSLMYW-LDPNLRYA--TREADIMEYAVNCHVITWERIVSHFDIFAFGH 172

Qy   106  F---REFKVLILAYAVCRLRHWWAIAITTAVTSAFLLAKVILSKLFSQGAFGYVLPIISF 161
             |   |:|||:::                            ::|: |:| :::|
Db   173  FWGWAMKALLIRSYGLC------WITSITWELTELF----------------FMHLLP-NF 210

Qy   162  ILAWIETWFLD 172
             || |    :|
Db   211  AECWWDQVILD 221
```

RESULT 11

H97002

probable integral membrane protein [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <KUR>
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: H97002
A;Accession: H97002
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359925; PMID:21359925
A;Accession: H97002
A;Cross-references: UNIPROT:Q97KT1; UNIPARC:UPI0000000CFCF; GB:AE001437; PIDN:AAK78811.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
A;Genetics:
A;Gene: CAC0835

```
Query Match             7.0%;   Score 83.5;   DB 2;   Length 352;
Best Local Similarity  19.2%;   Pred. No. 4.1;
Matches  38;   Conservative  35;   Mismatches  50;   Indels  75;   Gaps  8;
```

RESULT 12

AE0302

sugar ABC transporter, permease protein YP02476 [imported] - Yersinia pestis (strain CO9:
C;Species: Yersinia pestis
C;Date: 02-Nov-2001
A;Accession: AE0302
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AE0302
A;Molecule type: DNA
A;Status: preliminary
A;Residues: 1-291 <KUR>
A;Cross-references: UNIPARC:UPI00000000CC19; UNIPROT:Q8ZDT0; GB:AL590842; PIDN:CAC91281.1;
C;Gene: YP02476
C;Superfamily: inner membrane protein

```
Query Match             6.9%;   Score 83;   DB 2;   Length 291;
Best Local Similarity  22.3%;   Pred. No. 3.6;
Matches  44;   Conservative  26;   Mismatches  57;   Indels  70;   Gaps  10;

Qy    38  ESYEGREKKGISDVRRTFCLFVTFD-----------------------LLFVTLLIWIIEL 74
              | |   :  :::   : :  :                        :||.| |::  |
Db   115  EFYNVRDKKTNEDMKKLIKAYLVQNKTLNMERIVKDEQIGGLSKSERIIAFLATVLLITS 174

Qy    75  NVVNGGI------ENTLEKEVMQ-----------YDYYSSYFDIF----LLAVFRFKVL 111
             : |||:      |: :                 :  : ||: |     ::| : :::
Db   175  VVNGAVIIRDREENTYYRYMYSPNSKFEYIFGNVIYNYIFSYIQLFIANSLMAIFGIYIG 234

Qy   112  I-----LAYAVCRLRHWWAIAILTTAVTSAF-----LLAKVILSKLFSQGAFGYVLPIIS 160
             :     | |  : |                      :|   :|: |:
Db   235  ISFLKMLSYGL-------ILTLVMTTFGTFIVCIFNKELYANMFSAA------IS 276

Qy   161  FILAWIETWFLDFKVLPQ 178
             :||:: |: |:::::|
Db   277  LILSLVGGTFINYKIMPE 294
```

RESULT 13

S34960

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Crithidia oncopelti mitochondrio
C;Species: mitochondrion Crithidia oncopelti
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S34960
R;Maslov, D.A.; Horvath, A.; Gwang II, K.; Kolesnikov, A.A.
submitted to the EMBL Data Library, October 1990
A;Reference number: S34958
A;Accession: S34960
A;Molecule type: DNA
A;Residues: 1-590 <MAS>
A;Cross-references: UNIPROT:O34192; UNIPARC:UPI00000BE400; EMBL:X56015; NID:g12879; PIDN
C;Genetics:

```
Qy    46  KGISDVRRTFCLFVTFDLLFVTLLIWIIELNVNGG-------------GGIENTL 84
                    :   :  | :  :|: |::   : |             ||:|:|
Db     9  KQVGSVLAASYLGYYSIFWFYFIWLAVSLSTEWRFVGIPTFNGLNNFILVWMQDPLFWKS 68

Qy    85  EKEVNQYDYSSYFDIFLLAVRFRFKVLILAYAVCRLRHWWAIAILTTAVTSAFLLAKV-- 141
                    |:    :     :  :|::::           ::        : : | :|:
Db    69  MLNVNRFLMY--YLPIVFISSFLF-----AFGLQKLKHG-----RTFVALSFLLANVSSG 116

Qy   142  -----ILSKLFSQGA-----FGYVLPIIS------FILAWIETW-----FL 171
                  |:|: |||::     ||  |:          :|:| ::      ||
Db   117  VAYSIVFSKIFSQNGPLNTFLYDWFGFTLFPWLTSPDFAMLSIALVVTWKFVGYYGLILFS 176

Qy   172  DFKVLPQE----AEEEN 184
              : : |:     ||::|
Db   177  GLNSIPKEIYSAAELDN 193
```

A;Gene: ND5
A;Genome: mitochondrion
A;genetic code: SGC6
A;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

```
Query Match    6.9%;   Score 83;   DB 1;   Length 590;
Best Local Similarity  23.9%;  Pred. No. 8.3;
Matches 32;  Conservative 23;  Mismatches 37;  Indels 42;  Gaps 7;

Qy   55 FCLFVTF-----DLL---FVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVF 106
           |:||:|      ||:    :|:|
Db   95 FILFYAFYIMYYDLMLKRFENIFWWFVLCHMFFI------LSYDYLTAYCGWELLGLF    146

Qy  107 RFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWI 166
              ||:|   ||:    |::|  :|
Db  147 SF-----FLISY-----FWYRFFALKFGFKSFFISKI------GDVLLLLSFVMTFI    187

Qy  167 ET------WFLDF 173
                   :|
Db  188 STGYGMINFYFVNF 201
```

RESULT 14
B29835
TraS protein - Escherichia coli plasmid pED208
C;Species: Escherichia coli
C;Date: 04-Aug-1988 #sequence_revision 04-Aug-1988 #text_change 09-Jul-2004
C;Accession: B29835
R;Finlay, B.B.; Paranchych, W.
J. Bacteriol. 166, 713-721, 1986
A;Title: Nucleotide sequence of the surface exclusion genes traS and traT from the IncF-
A;Reference number: A29835; MUID:8622783; PMID:3011738
A;Accession: B29835
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-186 <FIN>
A;Cross-references: UNIPROT:P14498; UNIPARC:UPI000001563
C;Genetics:
C;Genome: plasmid

```
Query Match    6.9%;   Score 82.5;   DB 1;   Length 186;
Best Local Similarity  23.8%;  Pred. No. 2.4;
Matches 40;   Indels 35;   Gaps 6;
```

A;Residues: 1-239 <TIGR>
A;Cross-references: UNIPROT:P47489; UNIPARC:UPI00000139AF7; GB:U39703; GB:L43967; NID:g3E
A;Experimental source: strain G-37
C;Genetic code: SGC3
C;Genetics:
A;Superfamily: Escherichia coli ygiH protein

```
Query Match    6.9%;   Score 82.5;   DB 1;   Length 239;
Best Local Similarity  21.7%;  Pred. No. 3.2;
Matches 33;  Conservative 26;  Mismatches 54;  Indels 39;  Gaps 8;

Qy   42 GREKKGISDVRRTF------------CLFVTFDLLFVTLL--WIIELNVNGGIENTLEKEVMQYD 92
            :|:                   :|       :|| |     |::
Db   42 GSKNPGATNSMRVFGLKIGFLVAIFDAFKGFFAFLLTWIL--FRFGLQGYLTEKYYQST      98

Qy   93 YYSSYFDIFLLAV------PRFK----VLILAYAVCRLRHWWAI------ALTTAVTSA 135
              |:|         |:||      |:|                     ALTTAVTSA
Db   99 YFLSYLSCFRAATIGHIFPLYFKPKGGKAIATTGGSLLAISLMWFLICLLIWIMITLITKY 158

Qy  136 FLLAKVILSKLFSQGAFGYVLPIISFILAWIE 167
           |||:                    :|:
Db  159 VSLASLITF------FVLAVI-ILIPWLD    180
```

RESULT 15
C64227
hypothetical protein homolog MG247 - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: C64227
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.;
,C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: C64227
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

```
Query Match    6.9%;   Score 82.5;   DB 2;   Length 186;
Best Local Similarity  23.8%;  Pred. No. 2.4;
Matches 31;  Conservative 24;  Mismatches 40;  Indels 35;  Gaps 6;

Qy   61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLL-----AVFRFKVLILAY 115
           |:||:|                               |:|
Db   44 FQLLFI----IFDIFINSNVR------DYH--YFDTFVIILGSNAFFSLVFLMSTY       87

Qy  116 AVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPII----------SFILAW 165
           |:|                                                    :|:
Db   88 NLVSLK---ISLGSEITEQSVLLKLVERKINSYGQFLMVVNAIVGCVLLSSGERFVAGL   143

Qy  166 IETWFLDFKV 175
           |:|::|
Db  144 GFSWFVTYLI 153
```

Search completed: October 31, 2006, 02:26:22
Job time : 75 secs

QM protein - protein search, using sw model

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GenCore version 5.1.9

Run on: October 31, 2006, 02:25:39 ; Search time 301 Seconds
(without alignments)
719.115 Million cell updates/sec

Title: US-10-063-518-14
Perfect score: 1195
Sequence: 1 MNHLPEDMENALTGSQSSHA..........EAGSEEAEEKQDSEKPLLEL 234
Scoring table: BLOSUM62
Searched: Gapop 10.0 , Gapext 0.5
Total number of hits satisfying chosen parameters: 2849598
2849598 seqs, 925015592 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt 7.2.*
  1: uniprot_sprot:*
  2: uniprot_trembl:*

SUMMARIES.

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1195	100.0	235	1	MENTO_HUMAN	O95772 homo sapien
2	1141.5	95.0	235	1	Q5U205_RAT	Q5u205 rattus norv
3	1134.5	94.9	235	2	MENTO_MOUSE	Q9dc13 mus musculu
4	1134.5	94.9	235	2	MENTO_MOUSE	Q3u8o7 mus musculu
5	1128.5	94.4	235	2	Q3U852_MOUSE	Q3u852 mus musculu
6	796	66.9	227	2	Q6DI38_BRARE	Q6di38 brachydanio
7	700.5	58.6	448	2	Q6DFR7_XENTR	Q6dfr7 xenopus tro
8	698.5	58.5	444	2	Q6PF40_XENLA	Q6pf40 xenopus lae
9	684	57.2	448	2	Q6GNT3_XENLA	Q6gnt3 xenopus lae
10	664	55.6	445	1	O14849_HUMAN	O14849 homo sapien
11	664	55.6	445	2	Q53Y53_HUMAN	Q53y53 homo sapien
12	656.5	54.9	446	2	MLN64_MOUSE	Q61542 mus musculu
13	656.5	54.9	446	2	Q54C3_MOUSE	Q54c3 m 3 days ne
14	656.5	54.9	446	1	MLN64_RAT	Q5u2t5 rattus norv
15	632	52.9	448	1	MLN64_BRARE	Q9df84 brachydanio
16	586.5	49.1	444	2	Q4S943_TETNG	Q4s943 tetraodon n
17	566	47.4	501	2	Q5RB70_PONPY	Q5rb70 pongo pygma
18	364.5	30.5	574	2	Q563D1_AEDAE	Q563d1 aedes aegyp
19	364.5	30.5	595	2	Q563D0_AEDAE	Q563d0 aedes aegyp
20	346	29.0	523	2	Q7Q1T3_ANOGA	Q7q1t3 anopheles g
21	343	28.7	545	2	Q8MZH4_DROME	Q8mzh4 drosophila
22	343	28.7	583	2	Q9W145_DROME	Q9w145 drosophila
23	342.5	28.7	131	2	Q4TH5_TETNG	Q4th5 tetraodon n
24	330	27.6	476	2	Q3V5Y6_BOMMO	Q3v5y6 bombyx mori
25	272	22.8	197	2	Q4SN2_TETNG	Q4sn2 tetraodon n
26	209.5	17.5	185	2	Q5BVU9_SCHJA	Q5bvu9 schistosoma
27	206.5	17.3	419	2	O60270_CAEBR	O60270 caenorhabdi
28	204	17.1	447	2	O19819_CAEEL	O19819 caenorhabdi
29	181.5	15.2	141	2	Q4SNJ3_TETNG	Q4snj3 tetraodon n
30	117	9.8	459	2	Q4F23_METBA	Q4f23 methanosarc
31	104.5	8.7	294	1	MLN64_SALFO	Q90zb9 salvelinus
32	102.5	8.6	348	2	Q97YQ0_SULSO	Q97yq0 sulfolobus
33	100.5	8.4	369	2	Q31ET4_THICR	Q31et4 thiomicrosp
34	99.5	8.3	1095	2	Q4N7C1_THEPA	Q4n7c1 theileria p
35	96.5	8.1	714	2	Q5LPT4_SILPO	Q5lpt4 silicibacte
36	95.5	8.0	493	2	Q37IK3_RHODOPSEUDO	Q37ik3 rhodopseudo
37	95	7.9	616	2	Q30SK2_THIDN	Q30sk2 thiomicrosp
38	93.5	7.8	424	2	Q9UZW1_PYRAB	Q9uzw1 pyrococcus
39	93.5	7.8	438	1	CLN3_MACFA	Q60hh0 macaca fasc
40	93.5	7.8	564	2	Q8HQ10_THRIM	Q8hq10 thrips imag
41	93.5	7.7	304	2	Q21X08_RHOPA	Q21x08 rhodopseudo
42	92	7.7	246	2	Q8DU10_STRMU	Q8du10 streptococc
43	91	7.6	651	2	Q7VFT4_HELHP	Q7vft4 helicobacte
44	91	7.6	651	2	Q3D8X6_STRAG	Q3d8x6 streptococc
45	91	7.6	651	2	Q3D2J8_STRAG	Q3d2j8 streptococc
46	91	7.6	651	2	Q8DUY5_STRAG	Q8duy5 streptococc
47	91	7.6	651	2	Q3K1B2_STRA1	Q3k1b2 streptococc
48	91	7.6	525	2	Q8DZX0_STRA5	Q8dzx0 streptococc
49	90.5	7.6	262	2	Q8E5M0_STRA3	Q8e5m0 streptococc
50	90.5	7.6	284	2	Q7NBJ4_MYCGA	Q7nbj4 mycoplasma
51	90.5	7.6	530	2	Q3WYL1_9ACTN	Q3wyl1 rubrobacter
52	90	7.5	401	2	Q54F03_DICDI	Q54f03 dictyosteli
53	90	7.5	233	2	Q36VR4_RHOPA	Q36vr4 rhodopseudo
54	89.5	7.5	367	2	O02038_CYACP	O02038 cyanea capi
55	89.5	7.5	376	2	Q6JCT3_9HEMI	Q6jct3 aleurodicus
56	89.5	7.5	478	2	Q8HEH8_9ACAR	Q8heh8 varroa dest
57	89.5	7.5	488	2	Q6JCT6_9HEMI	Q6jct6 aleurodicus
58	89.5	7.4	387	2	Q60INO_CAEBR	Q60ino caenorhabdi
59	89	7.4	387	2	Q840W7_STRMU	Q840w7 streptococc
60	89	7.4	651	2	Q7RTB5_PLAYO	Q7rtb5 plasmodium
61	89	7.4	651	2	Q568R5_BRARE	Q568r5 brachydanio
62	89	7.4	897	2	Q3DLX9_STRAG	Q3dlx9 streptococc
63	89	7.4	473	2	Q5K830_CRYNE	Q5k830 cryptococcu
64	88.5	7.4	384	2	O6WNV4_RANCA	O6wnv4 rana catesb
65	88	7.4	453	2	O4C173_CROWT	O4c173 crocosphaer
66	88	7.4	755	2	O60QU6_CAEBR	O60qu6 caenorhabdi
67	87.5	7.3	396	2	Q4HDY8_CAMCO	Q4hdy8 campyloobact
68	87.5	7.3	891	2	Q5ZM65_CHICK	Q5zm65 gallus gall
69	87	7.3	613	2	Q3KQH5_XENLA	Q3kqh5 xenopus lae
70	87	7.3	360	2	Q6Q4E5_XENLA	Q6q4e5 xenopus lae
71	87	7.3	339	2	Q7RRS2_PLAYO	Q7rrs2 plasmodium
72	87	7.3	337	2	Q6GN42_XENLA	Q6gn42 xenopus lae
73	87	7.3	336	2	Q8PYM2_METMA	Q8pym2 methanosarc
74	86.5	7.3	331	2	Q55IJ0_CRYNE	Q55ij0 cryptococcu
75	86	7.2	174	2	Q5IJ0_GLOVI	Q5ij0 gloeobacter
76	86	7.2	1453	2	Q7NLI9_GLOVI	Q7nli9 gloeobacter
77	86	7.2	1056	2	Q7ZZ05_CAEEL	Q7zz05 caenorhabdi
78	86	7.2	1050	2	Q4YS44_PLABE	Q4ys44 plasmodium
79	86	7.2	438	2	Q95086_HUMAN	Q95086 homo sapien
80	85.5	7.2	396	2	Q4Y634_PLACH	Q4y634 plasmodium
81	85.5	7.2	451	2	Q95089_HUMAN	Q95089 homo sapien
82	85.5	7.2	438	2	Q2TA70_HUMAN	Q2ta70 homo sapien
83	85.5	7.2	473	2	Q9PME5_CAMJE	Q9pme5 campylobact
84	85.5	7.2	473	1	CLN3_HUMAN	Q13286 homo sapien
85	85.5	7.2	451	2	Q47H59_DECAR	Q47h59 dechloromon
86	85.5	7.2	707	2	Q549S9_HUMAN	Q549s9 homo sapien
87	85.5	7.2	302	2	P48651_BOVIN	P48651 bos taurus
88	85.5	7.2	747	2	Q93GL8_SALTY	Q93gl8 salmonella
89	85.5	7.2	473	2	Q35HJ0_9BRAD	Q35hj0 bradyrhizob
90	85.5	7.2	756	2	Q9SF17_ARATH	Q9sf17 arabidopsis
91	85.5	7.2	720	2	Q612C1_BACAN	Q612c1 bacillus an
92	85.5	7.2	897	2	Q51531_BORBU	Q51531 borrelia bu
93	85.5	7.2	912	2	Q51531_BORBU	Q51531 borrelia bu
94	85.5	7.1	707	2	Q82GJ8_STRAW	Q82gj8 streptomyce
95	85	7.1	610	2	Q4B5Q6_9BURK	Q4b5q6 polaromonas
96	85	7.2	304	2	Q4ITL6_AZOVI	Q4itl6 azotobacter
97	85	7.2	301	2		
98	85	7.2	2515	2		
99	85	7.1	336	2		
100	85	7.1	377	2		
101	85	7.1	302	2		
102	85	7.1	797	2		
103	85	7.1	793	2		
104	84.5	7.1	412	2		

Records 105–177

#	%id	score	len	f	Accession	Organism
105	84.5	7.1	430	2	Q5ZTB7_LEGPH	legionella
106	84.5	7.1	471	2	PTSS1_CRIGR	criceptulus
107	84.5	7.1	473	1	PTSS1_MOUSE	mus musculu
108	84.5	7.1	473	1	Q99LH2	mus musculu
109	84.5	7.1	473	2	Q3UV14_MOUSE	mus musculu
110	84.5	7.1	487	2	Q5PQL5_RAT	rattus norv
111	84.5	7.1	620	2	Q6A0E5_MOUSE	mus musculu
112	84.5	7.1	886	2	Q3Q9T9_9GAMM	shewanella
113	84.5	7.1	892	2	Q2RAN1_ORYSA	oryza sativ
114	84.5	7.1	895	2	Q9JF90_VACCT	vaccinia vi
115	84.5	7.1	1118	2	Q2TW55_ASPOR	aspergillus
116	84.5	7.1	1118	2	Q65U88_MANSM	mannheimia
116	84.5	7.0	3848	2	Q5HSR1_CAMJR	campylobact
117	84.5	7.0	396	2	Q5CUX5_CRYPV	cryptospori
117	84	7.0	468	2	Q42828_DESHA	desulfitoba
118	84	7.0	469	2	Q9HJK8_THEAC	thermoplasm
119	84	7.0	493	2	Q7TSH7_MOUSE	m potassium
119	84	7.0	809	2	Q43RP5_SOLUS	solibacter
120	84	7.0	1700	2	Q75JN1_DICDI	dictyosteli
121	84	7.0	170	2	Q4YS32_PLABE	plasmodium
122	84	7.0	275	2	Q8XIT3_CLOPE	clostridium
123	83.5	7.0	276	2	Q4D766_TRYCR	trypanosoma
124	83.5	7.0	303	2	Q6FNB8_CANGA	candida gla
125	83.5	7.0	322	2	Q8LB40_ARATH	arabidopsis
126	83.5	7.0	352	2	Q97KM1_CLOAB	clostridium
127	83.5	7.0	355	2	Q6KI24_MYCMO	mycoplasma
128	83.5	7.0	380	2	Q97C55_THEVO	thermoplasm
129	83.5	7.0	429	2	Q5E5F1_VIBF1	vibrio fisc
130	83.5	7.0	490	2	Q9CTA9_MOUSE	mus musculu
131	83.5	7.0	503	2	Q36846_MARHY	marinobacte
132	83.5	7.0	599	2	Q6PCX2_MOUSE	mus musculu
133	83.5	7.0	662	2	Q88P20_PSEPK	pseudomonas
134	83.5	7.0	834	2	Q9JHF5_MOUSE	mus musculu
135	83.5	7.0	834	2	Q9JL12_MOUSE	mus musculu
136	83.5	7.0	834	2	Q91W06_MOUSE	mus musculu
137	83.5	7.0	1034	2	Q72ZB9_TRYCR	trypanosoma
138	83.5	7.0	2483	2	Q5CH29_CRYHO	cryptospori
139	83	7.0	238	2	Q6YR96_ONYPE	onion yello
140	83	7.0	248	2	Q8GCS6_EUBAC	eubacterium
141	83	7.0	280	2	Q82DT0_NITOC	nitrosococc
142	83	6.9	291	2	Q8ZDT0_YERPE	yersinia pe
143	83	6.9	438	1	Q5XIH8_RAT	rattus norv
144	83	6.9	589	2	Q7TMW1_MOUSE	mus musculu
145	83	6.9	590	2	Q34192_CRION	crithidia o
146	83	6.9	738	2	Q30S24_THIDN	thiomicrosp
147	83	6.9	1056	2	Q8C2VI_MOUSE	mus musculu
148	83	6.9	1388	2	Q5DU28_MOUSE	mus musculu
149	83	6.9	2661	2	Q7RMS4_PLAYO	plasmodium
150	83	6.9	174	1	P97231_9ENTR	escherichia
151	82.5	6.9	186	2	TRAS2_ECOLI	salmonella
152	82.5	6.9	186	1	P14498_SALTI	salmonella
153	82.5	6.9	218	2	Q3IQR1_NATPD	natronomona
154	82.5	6.9	239	1	Y247_MYCGE	mycoplasma
155	82.5	6.9	255	2	Q36E00_9GAMM	shewanella
156	82.5	6.9	341	2	Q56918_YEREN	yersinia en
157	82.5	6.9	367	2	Q8HCX3_9ACAR	varroa dest
158	82.5	6.9	389	2	Q5FL80_LACAC	lactobacill
159	82.5	6.9	406	2	Q51180_LACAC	lactococcus
160	82.5	6.9	419	2	O19134_RABIT	oryctolagus
161	82.5	6.9	422	2	O87249_9LACT	lactococcus
162	82.5	6.9	471	2	O333G1_9CAUD	bacteriopha
163	82.5	6.9	510	2	Q950M6_9FUNG	cricetulus
164	82.5	6.9	604	2	Q9QW77_CRIGR	rhizophydiu
165	82.5	6.9	717	2	Q8RHJ3_FUSNN	fusobacteri
166	82.5	6.9	781	2	P09130_ECOLI	escherichia
167	82.5	6.9	891	2	Q4U8B8_THEAN	theileria a
168	82.5	6.9	891	2	Q57223_9POXV	vaccinia vi
169	82.5	6.9	891	2	Q49PJ1_9POXV	vaccinia vi
170	82.5	6.9	891	2	Q6J3A9_9POXV	vaccinia vi
171	82.5	6.9	892	2	Q80DW2_COWPX	cowpox viru
172	82.5	6.9	894	2	Q6RZH3_9POXV	rabbitpox v
173	82.5	6.9	1022	2	Q80QM10_COWPX	cowpox viru
174	82.5	6.9	156	2	Q88VO0_LACPL	lactobacill
175	82	6.9	161	2	O8I501_9HEPC	hepatitis c
176	82	6.9	—	2	O8I501_9HEPC	hepatitis c
177	82	6.9	—	2	Q69UD2_ORYSA	oryza sativ

Records 178–250

#	f	Accession	Organism	%id	score	len	f	Accession	Organism
178	2	Q6C0H8_YARLI	yarrowia li	82	6.9	201	2	Q45PY3_9CAUD	bacteriopha
179	2	RGP1_MOUSE	mus musculu	82	6.9	228	2	Q5ESD8_VIBF1	vibrio fisc
180	2	P46061	mus musculu	82	6.9	301	2	Q8RLZ3_HAEIN	haemophilus
181	2	Q9N2B5_MOUSE	m rangapl p	82	6.9	303	2	Q89L18_BRAJA	bradyrhizob
182	2	Q8C2E3_MOUSE	mus musculu	82	6.9	316	2	Q61RL6_CAEBR	caenorhabdi
183	2	Q91Y82_MOUSE	mus musculu	82	6.9	382	2	Q61F16_MOUSE	mus musculu
184	2	Q6ZPH4_MOUSE	mus musculu	82	6.9	384	2	Q50H98_PORGI	porphyromon
185	2	Q8PXU3_METMA	methanosarc	82	6.9	387	2	Q50H98_PORGI	porphyromon
186	2	Q4HJJ3_CAMLA	campylobact	82	6.9	461	2	Q50HU1_PORGI	porphyromon
187	2	Q4JCD0_SULAC	sulfolobus	82	6.9	472	2	Q30PJ9_THIDN	thiomicrosp
188	2	Q6CDE6_YARLI	yarrowia li	82	6.9	564	2	Q6AHB8_LEIXX	leifsonia x
189	2	Q81564_PLAF7	emericella	82	6.9	581	2	Q70J50_HAEIN	haemophilus
190	2	P78576_EMENI	emericella	82	6.9	587	2	Q2UHP4_ASPOR	aspergillus
191	2	Q5AS02_EMENI	emericella	82	6.9	589	2	Q4RON5_TETNG	tetraodon n
192	2	Q9KIA9	escherichia	82	6.9	589	1	RGP1_MOUSE	mus musculu
193	2	Q51D23_ENTHI	entamoeba h	82	6.9	646	2	P46061	mus musculu
194	2	Q9B893_9TREM	schistosoma	82	6.9	647	2	Q9N2B5_MOUSE	m rangapl p
195	2	Q2X2A4_9GAMM	shewanella	82	6.9	819	2	Q8C2E3_MOUSE	mus musculu
196	2	Q2Z6H6_SHEPU	shewanella	82	6.9	989	2	Q91Y82_MOUSE	mus musculu
197	2	Q8CDI4_MOUSE	mus musculu	82	6.9	1031	1	Q6ZPH4_MOUSE	mus musculu
198	2	Q2Z083_9GAMM	uncultured	82	6.9	1466	2	Q8PXU3_METMA	methanosarc
199	2	Q9CNP3_PASMU	pasteurella	82	6.9	1466	2	Q4HJJ3_CAMLA	campylobact
200	2	Q9H7E5_HUMAN	homo sapien	82	6.9	283	2	Q4JCD0_SULAC	sulfolobus
201	2	Q72CJ7_DESVH	desulfovibr	82	6.9	297	2	Q6CDE6_YARLI	yarrowia li
202	2	Q4VBD2_MOUSE	mus musculu	82	6.9	306	2	Q81564_PLAF7	emericella
203	2	Q6PAH4_MOUSE	mus musculu	81.5	6.8	306	2	P78576_EMENI	emericella
204	2	Q35934_9MOLU	mus musculu	81.5	6.8	311	2	Q5AS02_EMENI	emericella
205	2	Q8C5B1_MOUSE	mus musculu	81.5	6.8	342	2	Q9KIA9	escherichia
206	2	Q7VRC0_BLOFL	blochmannia	81.5	6.8	349	1	Q51D23_ENTHI	entamoeba h
207	2	Q4EJ15_LISMO	listeria mo	81.5	6.8	352	2	Q9B893_9TREM	schistosoma
208	2	Q80309_BRARE	brachydanio	81.5	6.8	311	2	Q2X2A4_9GAMM	shewanella
209	2	Q9NVS8_HUMAN	homo sapien	81.5	6.8	342	2	Q2Z6H6_SHEPU	shewanella
210	2	Q6P126_HUMAN	homo sapien	81.5	6.8	349	2	Q8CDI4_MOUSE	mus musculu
211	2	Q7Z748_HUMAN	homo sapien	81.5	6.8	352	2	Q2Z083_9GAMM	uncultured
212	2	Q67UQ9_ORYSA	oryza sativ	81.5	6.8	391	2	Q9CNP3_PASMU	pasteurella
213	2	Q8DLB4_SYNEL	synechococc	81.5	6.8	414	2	Q9H7E5_HUMAN	homo sapien
214	2	Q8B3Y6_ECOLI	escherichia	81.5	6.8	438	2	Q72CJ7_DESVH	desulfovibr
215	2	Q775R6_CAMPS	camelpox vi	81.5	6.8	438	2	Q4VBD2_MOUSE	mus musculu
216	2	Q8VZP5_CAMPS	camelpox vi	81.5	6.8	447	2	Q6PAH4_MOUSE	mus musculu
217	2	Q755K6_ASHGO	ashbya goss	81.5	6.8	463	2	Q35934_9MOLU	mus musculu
218	1	Q4SGQ6_TETNG	tetraodon n	81.5	6.8	465	2	Q8C5B1_MOUSE	mus musculu
219	2	Q7R386_GIALA	giardia lam	81.5	6.8	519	2	Q7VRC0_BLOFL	blochmannia
220	2	Q55S96_CRYNE	cryptococcu	81.5	6.8	519	2	Q4EJ15_LISMO	listeria mo
221	2	Q5KGP3_CRYNE	cryptococcu	81.5	6.8	577	2	Q80309_BRARE	brachydanio
222	2	Q2NFQ6_9EURY	methanospha	81.5	6.8	577	2	Q9NVS8_HUMAN	homo sapien
223	2	Q2KY24_BORAV	bordetella	81.5	6.8	645	1	Q6P126_HUMAN	homo sapien
224	2	Q92G69_ARATH	arabidopsis	81.5	6.8	716	2	Q7Z748_HUMAN	homo sapien
225	2	Q6D043_ERWCT	erwinia car	81.5	6.8	735	2	Q67UQ9_ORYSA	oryza sativ
226	2	Q4MPN6_BACCE	bacillus ce	81.5	6.8	892	2	Q8DLB4_SYNEL	synechococc
227	2	Q63E77_BACC2	bacillus ce	81.5	6.8	892	2	Q8B3Y6_ECOLI	escherichia
228	2	Q5AL74_CANAL	candida alb	81.5	6.8	1092	2	Q775R6_CAMPS	camelpox vi
229	2	YOU1_CAEEL	caenorhabdi	81.5	6.8	1472	1	Q8VZP5_CAMPS	camelpox vi
230	2	Q5A405_CANAL	candida alb	81.5	6.8	1480	2	Q755K6_ASHGO	ashbya goss
231	2	Q63E7	bacillus ce	81.5	6.8	1659	2	Q4SGQ6_TETNG	tetraodon n
232	2	Q63E7	bacillus ce	81	6.8	1692	2	Q7R386_GIALA	giardia lam
233	2	Q5AL74	candida alb	81	6.8	216	2	Q55S96_CRYNE	cryptococcu
234	2	O87249	lactococcus	81	6.8	285	2	Q5KGP3_CRYNE	cryptococcu
235	2	O51180	lactobacill	81	6.8	385	2	Q2NFQ6_9EURY	methanospha
236	2	O333G1	bacteriopha	81	6.8	410	2	Q2KY24_BORAV	bordetella
237	2	Q950M6	cricetulus	81	6.8	483	2	Q92G69_ARATH	arabidopsis
238	2	Q9QW77	rhizophydiu	81	6.8	486	2	Q6D043_ERWCT	erwinia car
239	2	Q8RHJ3	fusobacteri	81	6.8	492	2	Q4MPN6_BACCE	bacillus ce
240	2	P09130	escherichia	80.5	6.8	510	2	Q63E77_BACC2	bacillus ce
241	2	Q4U8B8	theileria a	80.5	6.8	520	1	Q5AL74_CANAL	candida alb
242	2	Q57223	vaccinia vi	80.5	6.8	532	2	YHB7_YEAST	saccharomyc
243	2	Q49PJ1	vaccinia vi	80.5	6.8	780	2	Q3H7U2_TRIER	trichodesmi
244	2	Q6J3A9	vaccinia vi	80.5	6.8	780	2	Q3H7U2_TRIER	trichodesmi
245	2	Q80DW2	cowpox viru	81	6.8	805	2	Q8XSV5_RALSO	ralstonia s
246	2	Q6RZH3	rabbitpox v	80.5	6.7	1174	2	Q8QRL8_9HEPC	hepatitis c
247	2	Q80QM10	cowpox viru	80.5	6.7	3010	2	P97066_9ENTR	salmonella
248	2	Q8GMU0	cowpox viru	80.5	6.7	174	2	Q2NIM4_9MOLU	salmonella
249	2	Q88VO0	lactobacill	80.5	6.7	240	2	Q2NIM4_9MOLU	aster yello
250	2	O8I501	hepatitis c	80.5	6.7	242	2	Q8TNE9_METAC	methanosarc
				80.5	6.7	248	2	Q3PSH1_NITHA	nitrobacter
				80.5	6.7	249	2	Q3PSH1_NITHA	nitrobacter
				80.5	6.7	284	2	Q56WV6_ARATH	arabidopsis
				80.5	6.7	322	2	Q56WV6_ARATH	arabidopsis

No	Score	E	Len	N	Accession	Organism
251	80.5	6.7	322	2	Q9SNE5_ARATH	arabidopsis
252	80.5	6.7	353	1	MTR1A_PHOSU	phodopus su
253	80.5	6.7	366	1	Q86KR8_DICDI	dictyosteli
254	80.5	6.7	396	1	BTN1_SCHPO	schizosacch
255	80.5	6.7	417	1	TNAB_PROVU	proteus vul
256	80.5	6.7	423	2	P28785	streptococc
257	80.5	6.7	463	2	Q4K188_STRPN	listeria mo
258	80.5	6.7	463	2	Q72204_LISMF	listeria mo
259	80.5	6.7	463	2	Q8Y988_LISMO	listeria mo
260	80.5	6.7	485	2	Q5EA23_XENLA	xenopus lae
261	80.5	6.7	485	2	Q5EAZ3	dictyosteli
262	80.5	6.7	486	2	Q54Z56_DICDI	chlamydia t
263	80.5	6.7	536	2	MVIN_CHLTR	malawimonas
264	80.5	6.7	536	2	Q9G861_9EUKA	chlamydia t
265	80.5	6.7	548	2	Q46378_PLAYO	plasmodium
266	80.5	6.7	554	2	Q7RC45_PLAYO	plasmodium
267	80.5	6.7	599	2	Q91ME6_9REOV	human rotav
268	80.5	6.7	644	1	Q4Y6E4_PLACH	plasmodium
269	80.5	6.7	644	2	Q6B2V3_YEAST	saccharomyc
270	80.5	6.7	716	2	Q5JBP7_ECOLI	saccharomyc
271	80.5	6.7	732	2	Q2TU08_ECOLI	escherichia
272	80.5	6.7	732	2	Q6SIZ5_ECOLI	escherichia
273	80.5	6.7	733	2	Q3YTF2_SHISS	escherichia
274	80.5	6.7	733	2	TRAD2_ECOLI	escherichia
275	80.5	6.7	738	1	P22708_ECOLI	escherichia
276	80.5	6.7	738	1	Q7AK62_9ZZZZ	shigella so
277	80.5	6.7	891	1	VP4A_VACCC	neurospora
278	80.5	6.7	891	1	P16715_VACCV	arabidopsis
279	80.5	6.7	891	2	Q76ZQ5_9POXV	arabidopsis
280	80.5	6.7	891	2	Q5IXQ4_MONPV	deinococcus
281	80.5	6.7	1687	2	Q8V4W5_MONPV	hepatitis c
282	80.5	6.7	1780	2	Q2UU23_ASPOR	caenorhabdi
283	80.5	6.7	103	2	Q7SC49_NEUCR	vaccinia vi
284	80.5	6.7	156	2	Q9ZT82_ARATH	monkeypox v
285	80.5	6.7	197	2	Q9RX39_DEIRA	vaccinia vi
286	80.5	6.7	238	2	Q5QTD8_HUMAN	monkeypox v
287	80.5	6.7	238	2	Q95KH1_MACFA	aspergillus
288	80.5	6.7	255	2	Q6V7H6_EAV	equine arte
289	80.5	6.7	280	2	Q4MTK3_BACCE	bacillus ce
290	80.5	6.7	280	2	Q635R8_BACCZ	bacillus ce
291	80.5	6.7	280	2	Q6HEF5_BACHK	bacillus th
292	80.5	6.7	280	2	Q819H0_BACCR	bacillus ce
293	80.5	6.7	280	2	Q73IV3_BACC1	bacillus ce
294	80.5	6.7	280	2	Q81MN0_BACAN	bacillus an
295	80.5	6.7	290	2	Q7A5Y6_STAAN	staphylococ
296	80.5	6.7	290	2	Q99UM2_STAAM	staphylococ
297	80.5	6.7	296	2	Q3EEG9_ACTSC	actinobacil
298	80.5	6.7	300	2	Q9C840_ARATH	arabidopsis
299	80.5	6.7	309	1	P40133_YEAST	saccharomyc
300	80.5	6.7	343	2	Q7USB9_RHOBA	rhodopirell
301	80.5	6.7	347	2	Q9FFM1_ARATH	arabidopsis
302	80.5	6.7	355	2	Q73JA5_TREDE	treponema d
303	80.5	6.7	359	2	Q7N4F8_PHOLL	photorhabdu
304	80.5	6.7	360	2	Q9H1X3_HUMAN	homo sapien
305	80.5	6.7	388	2	Q58427_PYRHO	pyrococcus
306	80.5	6.7	418	2	Q3P007_9GAMM	shewanella
307	80.5	6.7	488	2	Q65O88_ORYSA	oryza sativ
308	80.5	6.7	540	2	Q6FX17_CANGA	candida gla
309	80.5	6.7	554	2	Q6PC93_USTMA	ustilago ma
310	80.5	6.7	650	2	Q69F8_ANOGA	anopheles g
311	80.5	6.7	661	2	Q75SY6_ASHGO	ashbya goss
312	80.5	6.7	680	2	Q4EKL7_LISMO	listeria mo
313	80	6.7	700	2	Q72OZ1_LISMO	listeria mo
314	80	6.7	700	2	Q4EKL7	listeria mo
315	80	6.7	893	2	Q4I7J8_GIBZE	gibberella
316	80	6.7	3010	2	Q9QIY9_9HEPC	hepatitis c
317	79.5	6.7	266	2	Q3SLE7_THIDA	thiobacillu
318	79.5	6.7	266	2	Q5IPF8_9RODE	perognathus
319	79.5	6.7	266	2	Q5IPF9_9RODE	perognathus
320	79.5	6.7	269	2	Q4EFC5_LISMO	listeria mo
321	79.5	6.7	269	2	Q72B0_LISMF	listeria mo
322	79.5	6.7	273	2	Q3WS44_9RHIZ	mesorhizobi
323	79.5	6.7	304	2	Q33ZM2_RHOPA	rhodopseudo

No	Score	E	Len	N	Accession	Organism
324	79.5	6.7	307	2	Q89NC2_BRAJA	bradyrhizob
325	79.5	6.7	367	2	Q8ESY3_OCEIH	oceanobacil
326	79.5	6.7	379	2	Q508J9_9RODE	perognathus
327	79.5	6.7	391	2	Q6TY96_9BILA	xiphinema a
328	79.5	6.7	392	2	Q2MDL9_VIVIN	viverricula
329	79.5	6.7	404	2	Q405X5_9RHOB	jannaschia
330	79.5	6.7	438	1	CLN3_CANFA	canis famil
331	79.5	6.7	463	2	Q92E13_LISIN	listeria in
332	79.5	6.7	468	2	Q30R92_THIDN	thiomicrosp
333	79.5	6.7	488	2	Q6QU70_ASPNG	aspergillus
334	79.5	6.7	491	1	VIEL_HCMVT	human cytom
335	79.5	6.7	546	2	P60815_RAT	rattus norv
336	79.5	6.7	549	2	Q422F3_PLABE	plasmodium
337	79.5	6.7	598	2	Q51954_BORHE	borrelia he
338	79.5	6.7	674	2	Q86P19_DROME	drosophila
339	79.5	6.7	688	2	Q6B208_DEBHA	debaryomyce
340	79.5	6.7	688	2	Q35Y20_9GAMM	shewanella
341	79.5	6.7	726	2	Q9EUJ3_SALET	salmonella
342	79.5	6.7	732	2	Q5J497_SALCH	salmonella
343	79.5	6.7	748	2	Q4WB47_ASPFU	aspergillus
344	79.5	6.7	784	2	Q9VYY0_DROME	drosophila
345	79.5	6.7	784	2	Q8KDB0_CHLTE	chlorobium
346	79.5	6.7	818	2	Q5HXC6_CAMJR	campylobact
347	79.5	6.7	886	2	Q4ALC7_9CHLB	chlorobium
348	79.5	6.7	1708	2	Q4LE27_HUMAN	homo sapien
349	79.5	6.7	3409	2	Q7SI27_NEUCR	neurospora
350	79.5	6.6	114	2	Q6VRR6_HELPY	helicobacte
351	79.5	6.6	238	2	Q3UWH0_MOUSE	m 15 days e
352	79	6.6	251	2	Q6M0I2_METMP	methanococc
353	79	6.6	288	2	Q3EEL5_ACTSC	actinobacil
354	79	6.6	300	2	Q80ZH3_9MURI	arvicanthis
355	79	6.6	308	2	Q3EEL5_ACTSC	actinobacil
356	79	6.6	312	2	Q6KH29_MYCMO	mycoplasma
357	79	6.6	323	2	Q7KSI9_DROME	drosophila
358	79	6.6	345	2	Q360Y1_9GAMM	shewanella
359	79	6.6	349	1	RNFD_BUCAP	buchnera ap
360	79	6.6	350	2	Q36RI0_MARHY	marinobacte
361	79	6.6	356	2	Q5X814_LEGPA	legionella
362	79	6.6	356	2	Q7MG43_VIBVY	vibrio vuln
363	79	6.6	363	2	Q4ZXH6_PSEU2	pseudomonas
364	79	6.6	364	2	Q887L9_PSESM	pseudomonas
365	79	6.6	365	2	Q6M0I2_METMP	caldicellul
366	79	6.6	366	2	Q2ZGP3_CALSA	caldicellul
367	79	6.6	367	2	Q2JTY0_9CYAN	cyanobacter
368	79	6.6	428	2	Q6NIE0_CORDI	corynebacte
369	79	6.6	484	2	Q5LA24_BACFN	bacteroides
370	79	6.6	770	2	Q64QD3_BACFR	bacteroides
371	79	6.6	770	2	Q5LA24_BACFN	bacteroides
372	79	6.6	828	2	Q4QD3_TETNG	tetraodon n
373	79	6.6	1232	2	Q3JBT9_NITOC	nitrosococc
374	79	6.6	1531	2	Q96195_HUMAN	homo sapien
375	79	6.6	1679	2	Q86TB3_HUMAN	homo sapien
376	79	6.6	1780	2	Q61T87_CAEBR	caenorhabdi
377	79	6.6	2751	2	Q4Y3S8_PLACH	plasmodium
378	79	6.6	3010	2	Q9J3H8_9HEPC	hepatitis c
379	78.5	6.6	3010	2	Q9QI20_9HEPC	hepatitis c
380	78.5	6.6	229	2	Q353U9_9GAMM	shewanella
381	78.5	6.6	232	1	Q466U5_METBA	methanosarc
382	78.5	6.6	239	1	Y350_MYCPN	mycoplasma
383	78.5	6.6	263	2	Q4Z3F6_PLABE	plasmodium
384	78.5	6.6	266	2	Q5IPE7_9RODE	perognathus
385	78.5	6.6	269	2	Q92DL5_LISIN	listeria in
386	78.5	6.6	292	2	Q3WQW4_9RHIZ	mesorhizobi
387	78.5	6.6	305	2	Q5V6V4_HALMA	haloarcula
388	78.5	6.6	313	2	Q345Q5_RHOPA	rhodopseudo
389	78.5	6.6	353	2	Q9L0B3_STRCO	streptomyce
390	78.5	6.6	358	2	Q4HJT2_CAMLA	campylobact
391	78.5	6.6	358	1	RNFD_HAEIN	haemophilus
392	78.5	6.6	366	2	Q4QJQ5_HAEI8	haemophilus
393	78.5	6.6	393	2	Q4EU11_LISMO	listeria mo
394	78.5	6.6	394	2	Q8A8F8_BACTN	bacteroides
395	78.5	6.6	395	2	Q5LE17_BACPN	bacteroides
396	78.5	6.6	382	2	Q64V54_BACFR	bacteroides

#			Len	N	Accession	Code	Organism
397	78.5	6.6	418	2	Q65LP8_BACLD	q65lp8	bacillus li
398	78.5	6.6	451	2	Q65UD5_MANSM	q65ud5	mannheimia
399	78.5	6.6	471	1	5H2A_CRIGR	5h2a	cricetulus
400	78.5	6.6	512	2	P18599	p18599	brucella su
401	78.5	6.6	512	2	Q8G1D7_BRUSU	q8g1d7	brucella su
402	78.5	6.6	538	2	Q4HFH8_CAMCO	q4hfh8	campylobact
403	78.5	6.6	546	2	Q3T1I6_RAT	q3t1i6	rattus norv
404	78.5	6.6	557	2	Q5CXU4_CRYPV	q5cxu4	cryptospori
405	78.5	6.6	587	2	Q3D365_STRAG	q3d365	streptococc
406	78.5	6.6	609	1	Q3DHN0_STRAG	q3dhn0	streptococc
407	78.5	6.6	666	1	KUP_STRA5	kup	streptococc
408	78.5	6.6	666	2	Q8DZI1_STRAG	q8dzi1	streptococc
409	78.5	6.6	666	2	Q3DMX9_STRAG	q3dmx9	streptococc
410	78.5	6.6	678	2	Q61710_MOUSE	q61710	mus musculu
411	78.5	6.6	681	2	Q769F4_HUMAN	q769f4	homo sapien
412	78.5	6.6	683	2	Q769F3_HUMAN	q769f3	homo sapien
413	78.5	6.6	689	2	Q3Q502_9GAMM	q3q502	shewanella
414	78.5	6.6	726	2	Q4UC59_THEAN	q4uc59	theileria a
415	78.5	6.6	766	1	ABCB9_HUMAN	abcb9	homo sapien
416	78.5	6.6	766	2	Q6P2Q0_HUMAN	q6p2q0	homo sapien
417	78.5	6.6	796	2	Q5W9G7_HUMAN	q5w9g7	homo sapien
418	78.5	6.6	867	2	Q4N908_THEPA	q4n908	theileria p
419	78.5	6.6	1308	2	Q4XVA2_PLACH	q4xva2	plasmodium
420	78.5	6.6	6473	2	Q8IKH9_PLAF7	q8ikh9	plasmodium
421	78	6.6	188	2	Q81YM2_BACAN	q81ym2	bacillus an
422	78	6.6	219	2	Q8W2Y0_ORYSA	q8w2y0	oryza sativ
423	78	6.6	226	2	Q7T829_9CORO	q7t829	infectious
424	78	6.6	240	2	Q9CPF6_PASMU	q9cpf6	pasteurella
425	78	6.6	245	2	P94625_CLODI	p94625	clostridium
426	78	6.6	252	1	Q6B8K2_GRATL	q6b8k2	gracilaria
427	78	6.6	259	2	Q9KD13_BACHD	q9kd13	bacillus ha
428	78	6.6	298	2	Q48BH2_PSE14	q48bh2	pseudomonas
429	78	6.6	299	2	Q2KXZ7_BORAV	q2kxz7	bordetella
430	78	6.6	321	2	Q96XC4_SULTO	q96xc4	sulfolobus
431	78	6.6	339	2	Q8D4K9_VIBVU	q8d4k9	vibrio vuln
432	78	6.6	345	2	Q22AV5_9GAMM	q22av5	shewanella
433	78	6.6	357	2	Q2ZAV5_9GAMM	q2zav5	shewanella
434	78	6.6	360	2	Y872_HAEIN	y872	haemophilus
435	78	6.6	382	2	Q6HMA8_BACHK	q6hma8	bacillus th
436	78	6.6	414	2	Q3N6A0_9DELT	q3n6a0	syntrophoba
437	78	6.6	428	2	Q97HC3_CLOAB	q97hc3	clostridium
438	78	6.6	431	2	Q951A3_TETTH	q951a3	tetrahymena
439	78	6.6	442	2	Q8TN61_METAC	q8tn61	methanosarc
440	78	6.6	452	2	Q8D5Y9_VIBVU	q8d5y9	vibrio vuln
441	78	6.6	471	1	Q9JRS0_ACTAC	q9jrs0	actinobacil
442	78	6.6	486	2	Q7MD08_VIBVY	q7md08	vibrio vuln
443	78	6.6	494	2	Q36DZ4_9GAMM	q36dz4	shewanella
444	78	6.6	545	2	Q42OY8_DESHA	q42oy8	desulfitoba
445	78	6.6	638	2	Q98M77_RHILO	q98m77	rhizobium l
446	78	6.6	641	2	Q7QGQ8_ANOGA	q7qgq8	anopheles g
447	78	6.6	650	2	Q2YZ60_STAAB	q2yz60	staphylococ
448	78	6.6	658	2	Q9LIC2_ARATH	q9lic2	arabidopsis
449	78	6.6	688	2	Q2ZO24_9CHLR	q2zo24	uncultured
450	78	6.6	748	2	Q6FSM9_CANGA	q6fsm9	candida gla
451	78	6.6	1042	2	Q3SDA8_PARTE	q3sda8	paramecium
452	78	6.6	1088	2	Q43RR2_SOLUS	q43rr2	solibacter
453	78	6.6	1297	1	Q9Y817_SCHPO	q9y817	schizosacch
454	78	6.6	2136	1	YCF2_MARPO	ycf2	marchantia
455	78	6.6	7180	1	RIAB_CVMJTH	riab	m replicase
456	77.5	6.5	176	2	Q976T7_SULTO	q976t7	sulfolobus
457	77.5	6.5	190	2	Q9KIA8_ECOLI	q9kia8	escherichia
458	77.5	6.5	263	2	Q4MQY0_BACCE	q4mqy0	bacillus ce
459	77.5	6.5	263	2	Q81I83_BACC1	q81i83	bacillus ce
460	77.5	6.5	266	2	Q73DX2_BACC1	q73dx2	bacillus ce
461	77.5	6.5	269	2	Q5IPF6_PERLO	q5ipf6	perognathus
462	77.5	6.5	269	2	Q3EXW2_BACTI	q3exw2	bacillus th
463	77.5	6.5	269	2	Q4EV75_LISMO	q4ev75	listeria mo
464	77.5	6.5	270	2	Q8Y8T5_LISMO	q8y8t5	listeria mo
465	77.5	6.5	270	2	Q8HIY1_PERLO	q8hiy1	perognathus
466	77.5	6.5	270	2	Q8HIY2_PERLO	q8hiy2	perognathus
467	77.5	6.5	270	2	Q8HIY3_PERLO	q8hiy3	perognathus
468	77.5	6.5	294	2	Q8ET30_OCEIH	q8et30	oceanobacil
469	77.5	6.5	299	2	Q66FT9_YERPS	q66ft9	yersinia ps

#			Len	N	Accession	Code	Organism
470	77.5	6.5	299	2	Q82AL1_YERPE	q82al1	yersinia pe
471	77.5	6.5	310	2	Q8D1I6_YERPE	q8d1i6	yersinia pe
472	77.5	6.5	327	2	Q9PQG1_UREPA	q9pqg1	ureaplasma
473	77.5	6.5	328	2	Q9K686_BACHD	q9k686	bacillus ha
474	77.5	6.5	328	2	Q42882_SCHPO	q42882	schizosacch
475	77.5	6.5	347	2	Q4AFU3_9CHLB	q4afu3	chlorobium
476	77.5	6.5	365	2	Q8R770_THETN	q8r770	thermoanaer
477	77.5	6.5	377	2	Q4R1V7_VARHI	q4r1v7	variola hi
478	77.5	6.5	377	2	Q4R1X9_VARHI	q4r1x9	variola hi
479	77.5	6.5	377	2	Q4R264_VARHI	q4r264	variola hi
480	77.5	6.5	377	2	Q4R2A7_VARHI	q4r2a7	variola hi
481	77.5	6.5	377	2	Q4R2P5_VARHI	q4r2p5	variola hi
482	77.5	6.5	379	2	Q4R2P6_VARHI	q4r2p6	variola hi
483	77.5	6.5	384	2	Q48008_PEROG	q48008	perognathus
484	77.5	6.5	392	2	Q2WUY0_CLOBE	q2wuy0	clostridium
485	77.5	6.5	416	2	Q8G7P7_BIFLO	q8g7p7	bifidobacte
486	77.5	6.5	422	2	Q9P6N5_SCHPO	q9p6n5	schizosacch
487	77.5	6.5	430	2	Q4YTQ0_PLABE	q4ytq0	plasmodium
488	77.5	6.5	440	2	Q9HKX6_THEAC	q9hkx6	thermoplasm
489	77.5	6.5	458	2	Q5WUJ7_LEGPL	q5wuj7	legionella
490	77.5	6.5	481	2	Q9ZY23_PEDMN	q9zy23	pedinomonas
491	77.5	6.5	483	2	Q4P6B0_USTMA	q4p6b0	ustilago ma
492	77.5	6.5	491	2	Q62XT1_BACLD	q62xt1	bacillus li
493	77.5	6.5	491	2	Q89180_VARV	q89180	variola vir
494	77.5	6.5	483	2	Q2R1U9_ORYSA	q2r1u9	oryza sativ
495	77.5	6.5	556	2	Q2R1U9_ORYSA	q2r1u9	oryza sativ
496	77.5	6.5	548	2	Q89232_VARV	q89232	variola vir
497	77.5	6.5	543	2	Q89180_VARV	q89180	variola vir
498	77.5	6.5	538	2	Q4XZG8_PLACH	q4xzg8	plasmodium
499	77.5	6.5	526	2	Q59P22_CANAL	q59p22	candida alb
500	77.5	6.5	512	2	Q8EKA1_SHEON	q8eka1	shewanella
501	77.5	6.5	512	2	Q3MXT8_9DELT	q3mxt8	syntrophoba
502	77.5	6.5	620	2	Q4RUC9_TETNG	q4ruc9	tetraodon n
503	77.5	6.5	676	2	P12129_ORYSA	p12129	oryza sativ
504	77.5	6.5	734	1	NU5C_ORYSA	nu5c	oryza sativ
505	77.5	6.5	788	2	Q4HPP2_CAMUP	q4hpp2	campylobact
506	77.5	6.5	892	1	Q2ZED8_CALSA	q2zed8	caldicellul
507	77.5	6.5	892	2	Q4K5I9_PSEF5	q4k5i9	pseudomonas
508	77.5	6.5	979	1	P33817_VARV	p33817	variola vir
509	77.5	6.5	1033	2	Q9QNI0_VARV	q9qni0	variola vir
510	77.5	6.5	1140	2	Q7MLV5_VIBVY	q7mlv5	vibrio vuln
511	77.5	6.5	1476	2	Q5BL65_XENTR	q5bl65	xenopus tro
512	77.5	6.5	1784	2	Q5CTR7_CRYPV	q5ctr7	cryptospori
513	77.5	6.5	1959	2	Q8ST66_DICDI	q8st66	dictyosteli
514	77	6.5	2141	2	Q25377_LOLOP	q25377	loligo opal
515	77	6.5	6680	2	Q5ZSB8_ORYSA	q5zsb8	oryza sativ
516	77	6.5	170	1	Q869H2_LYMST	q869h2	lymnaea sta
517	77	6.5	160	2	Q5CXT7_CRYPV	q5cxt7	cryptospori
518	77	6.5	170	2	Q3EF80_ACTSC	q3ef80	actinobacil
519	77	6.5	191	2	Q72UC4_LEPIC	q72uc4	leptospira
520	77	6.5	200	2	Q8FOQ4_LEPIN	q8foq4	leptospira
521	77	6.5	226	2	Q3VS16_PROAE	q3vs16	prosthecoch
522	77	6.4	249	2	Q3LWE2_CHLS6	q3lwe2	chlorobium
523	77	6.4	255	2	Q33VA0_9GAMM	q33va0	shewanella
524	77	6.4	286	2	Q22645_9GAMM	q22645	shewanella
525	77	6.4	286	2	Q98VN5_EAV	q98vn5	equine arte
526	77	6.4	287	2	Q8U03O_BACTI	q8u03o	bacillus th
527	77	6.4	288	2	Q6I082_BACAN	q6i082	bacillus an
528	77	6.4	288	2	Q73A28_BACC1	q73a28	bacillus ce
529	77	6.4	315	2	Q54LT2_DICDI	q54lt2	dictyosteli
530	77	6.4	332	2	Q3GB03_9FIRM	q3gb03	syntrophomo
531	77	6.4	346	2	Q4HFE7_CAMCO	q4hfe7	campylobact
532	77	6.4	353	2	Q9XTH3_CAEEL	q9xth3	caenorhabdi
533	77	6.4	361	2	Q2NSZ8_SODGL	q2nsz8	sodalis glo
534	77	6.4	379	1	MTR1A_MOUSE	mtr1a	mus musculu
535	77	6.4	379	2	Q61184_LISMO	q61184	listeria mo
536	77	6.4	383	2	Q4EL37_LISMO	q4el37	listeria mo
537	77	6.4		2	Q8WEK6_THOTA	q8wek6	thomomys ta
538	77	6.4		2	Q8TZC2_METKA	q8tzc2	methanopyru

No.	Score		Length	N	Accession	Organism
543	77	6.4	386	2	Q7MXQ0_PORGI	porphyromon
544	77	6.4	419	2	P94949_METKA	methanopyru
545	77	6.4	423	2	Q71XS8_LISMF	listeria mo
546	77	6.4	430	2	Q8U1Z6_PYRFU	pyrococcus
547	77	6.4	435	2	Q73RD9_TREDE	treponema d
548	77	6.4	444	2	Q6GD70_STAAS	staphylococc
549	77	6.4	444	2	Q8NYX5_STAAW	staphylococc
550	77	6.4	473	2	Q3GS79_9GAMM	psychrobact
551	77	6.4	477	2	Q2SJ67_HAHCH	hahella che
552	77	6.4	481	2	Q4WQW3_ASPFU	aspergillus
553	77	6.4	490	2	O14670_HUMAN	homo sapien
554	77	6.4	491	2	Q9T251_PHYIN	phytophthor
555	77	6.4	505	2	Q4U156_THEAN	theileria a
556	77	6.4	519	2	Q9ASQ7_ARATH	arabidopsis
557	77	6.4	537	2	Q518N5_ENTHI	entamoeba h
558	77	6.4	559	2	Q9AAX4_CAUCR	caulobacter
559	77	6.4	590	1	NU5M_TRYBB	trypanosoma
560	77	6.4	606	2	Q2IFP2_9DELT	anaeromyxob
561	77	6.4	616	2	Q5W2R7_SULIS	sulfolobus
562	77	6.4	650	2	Q5HCQ6_STAAC	staphylococc
563	77	6.4	650	2	Q6G633_STAAS	staphylococc
564	77	6.4	650	2	Q6GDG1_STAAR	staphylococc
565	77	6.4	650	2	Q7A374_STAAN	staphylococc
566	77	6.4	650	2	Q8NUK4_STAAW	staphylococc
567	77	6.4	650	2	Q99QZ7_STAAM	staphylococc
568	77	6.4	722	2	Q632R1_BACCZ	bacillus ce
569	77	6.4	738	2	Q8L838_ARATH	arabidopsis
570	77	6.4	789	1	FTSK_STAAW	staphylococc
571	77	6.4	789	1	FTSK_STAAS	staphylococc
572	77	6.4	836	2	Q7Z1F2_PLAFA	plasmodium
573	77	6.4	877	2	Q750H8_ASHGO	ashbya goss
574	77	6.4	991	2	Q81330_ARATH	arabidopsis
575	77	6.4	1024	2	Q7Z1F1_PLAFA	plasmodium
576	77	6.4	1024	2	Q8IKZ6_PLAF7	plasmodium
577	77	6.4	1025	2	Q25693_PLAFA	plasmodium
578	77	6.4	1117	2	Q9M133_ARATH	arabidopsis
579	77	6.4	1117	2	Q44PG0_CHILI	chlorobium
580	77	6.4	1137	2	Q6FTR9_CANGA	candida gla
581	77	6.4	1477	2	Q92U84_ARATH	arabidopsis
582	77	6.4	1500	2	Q60WH4_CAEBR	caenorhabdi
583	77	6.4	1814	2	Q68788_9HEPC	hepatitis c
584	77	6.4	3010	2	Q81757_9HEPC	hepatitis c
585	77	6.4	3010	2	Q9J3G4_9HEPC	hepatitis c
586	77	6.4	3013	2	Q6J6P5_9HEPC	hepatitis c
587	77	6.4	4416	2	Q9J3F3_9CORO	murine hepa
588	77	6.4	4416	2	Q9J3F8_9CORO	murine hepa
589	77	6.4	7124	1	R1AB_CVM2	murine hepa
590	76.5	6.4	189	2	Q9PYA3_9ROCO	m replicase
591	76.5	6.4	234	2	Q3WSO1_9RHIZ	mesorhizobi
592	76.5	6.4	253	2	Q3W1WO_9ACTO	frankia sp.
593	76.5	6.4	266	2	Q5IPE6_PERLO	perognathus
594	76.5	6.4	278	2	Q5IPE8_PERLO	perognathus
595	76.5	6.4	281	2	Q8SKS9_9BILA	ancylostoma
596	76.5	6.4	282	2	Q92WV5_RHIME	rhizobium m
597	76.5	6.4	342	1	Y0E8_YEAST	saccharomyc
598	76.5	6.4	342	2	Q7Z290_CAEEL	caenorhabdi
599	76.5	6.4	352	1	RNFD_SALTI	salmonella
600	76.5	6.4	352	2	Q8ZPN3_SALMO	salmonella
601	76.5	6.4	352	2	Q57P11_SALCH	salmonella
602	76.5	6.4	352	2	Q5PIC8_SALPA	salmonella
603	76.5	6.4	358	2	Q3Y919_CRYGA	cryptococcu
604	76.5	6.4	379	1	CYB_DIPOR	dipodomys o
605	76.5	6.4	379	2	Q9GBY7_OCHPA	ochotona pa
606	76.5	6.4	379	2	Q50803_9RODE	perognathus
607	76.5	6.4	379	2	Q50BJ5_PERLO	perognathus
608	76.5	6.4	379	2	Q50BL8_9RODE	dipodomys m
609	76.5	6.4	380	2	Q8HNI7_PRANA	praomys nat
610	76.5	6.4	387	2	Q3VX84_PROAE	prosthecoch
611	76.5	6.4	391	2	Q4SIZ9_TETNG	tetraodon n
612	76.5	6.4	395	2	Q8KHK2_PSEAE	pseudomonas
613	76.5	6.4	415	2	Q5UE97_ECOLI	escherichia
614	76.5	6.4	415	2	Q7UB13_SHIFL	shigella fl
615	76.5	6.4	415	2	Q83PL5_SHIFL	shigella fl

No.	Score		Length	N	Accession	Organism
616	76.5	6.4	438	1	CLN3_MOUSE	mus musculu
617	76.5	6.4	439	2	Q5LBQ8_BACFN	bacteroides
618	76.5	6.4	439	2	Q64SN0_BACFR	bacteroides
619	76.5	6.4	451	2	Q660T8_BORGA	borrelia ga
620	76.5	6.4	453	2	Q6ZGZ4_ORYSA	oryza sativ
621	76.5	6.4	462	2	Q82V00_NITEU	nitrosomona
622	76.5	6.4	468	1	YDBM_CAEEL	caenorhabdi
623	76.5	6.4	468	2	Q3S1M1_CAEEL	caenorhabdi
624	76.5	6.4	490	2	Q6SX39_HCMV	human cytom
625	76.5	6.4	491	2	Q6SWP6_HCMV	human cytom
626	76.5	6.4	500	1	FLVC2_HUMAN	homo sapien
627	76.5	6.4	526	2	Q96ZH3_SULTO	sulfolobus
628	76.5	6.4	526	2	Q9UP13_HUMAN	homo sapien
629	76.5	6.4	528	2	Q7VP70_HAEDU	haemophilus
630	76.5	6.4	538	2	Q9PIV5_CAMJE	campylobact
631	76.5	6.4	538	2	Q9HWZ4_CAMJR	campylobact
632	76.5	6.4	555	2	Q53ZT9_HUMAN	homo sapien
633	76.5	6.4	560	2	Q8NBG4_HUMAN	homo sapien
634	76.5	6.4	560	2	Q627P1_CAEBR	caenorhabdi
635	76.5	6.4	584	2	Q72EJ6_HUMAN	homo sapien
636	76.5	6.4	589	2	Q2V4K0_ARATH	arabidopsis
637	76.5	6.4	614	2	Q92LN1_HELPJ	helicobacte
638	76.5	6.4	614	2	Q577U9_BRUAB	brucella ab
639	76.5	6.4	614	2	Q8FWB2_BRUSU	brucella su
640	76.5	6.4	615	2	Q2YKG7_BRUA2	brucella ab
641	76.5	6.4	649	2	Q5JF60_PYRKO	pyrococcus
642	76.5	6.4	666	2	Q6KZL4_PICTO	picrophilus
643	76.5	6.4	687	2	Q3D5N7_STRAG	streptococc
644	76.5	6.4	743	2	O74520_SCHPO	schizosacch
645	76.5	6.4	775	2	Q8XN80_CLOPE	clostridium
646	76.5	6.4	839	2	Q4N6A4_THEPA	theileria p
647	76.5	6.4	902	2	Q918C9_CHICK	gallus gall
648	76.5	6.4	909	2	Q3XN69_9PROT	magnetococc
649	76.5	6.4	909	2	Q81504_9HEPC	hepatitis c
650	76.5	6.4	925	2	Q6MT09_MYCMS	mycoplasma
651	76.5	6.4	1034	2	Q8PXL0_METMA	methanosarc
652	76.5	6.4	1141	2	Q6V7I5_EAV	equine arte
653	76.5	6.4	1228	2	Q2LYI0_9DELT	syntrophus
654	76.5	6.4	1485	2	Q2RFN9_MOOTH	moorella th
655	76.5	6.4	1641	2	Q3NBS3_9PROT	nitrosomona
656	76	6.4	156	2	Q8ELU4_OCEIH	oceanobacil
657	76	6.4	201	2	Q9ZZH9_MESAU	mesocricetu
658	76	6.4	210	2	Q3B337_PELLD	pelodictyon
659	76	6.4	210	1	NU2M_LOCMI	locusta mig
660	76	6.4	264	2	Q4H7X1_9DEIO	deinococcus
661	76	6.4	272	2	Q3LRX3_TARGR	taricha gra
662	76	6.4	292	2	Q21933_CAEEL	caenorhabdi
663	76	6.4	325	2	Q9JRS2_ACTAC	actinobacil
664	76	6.4	328	2	Q88HG7_PSEPK	pseudomonas
665	76	6.4	346	2	Q2Q1L3_9NEOP	grylloblatt
666	76	6.4	346	2	Q85002_STREN	streptococc
667	76	6.4	393	2	Q72SX4_LEPIC	leptospira
668	76	6.4	425	2	Q8F2K0_LEPIN	leptospira
669	76	6.4	425	2	Q38SJ6_9TRYP	trypanosoma
670	76	6.4	438	2	Q32EF8_EPIFL	epidermophy
671	76	6.4	446	2	Q852P3_PERFR	clostridium
672	76	6.4	461	2	Q6NXT6_HUMAN	homo sapien
673	76	6.4	474	2	Q7QWH6_GIALA	giardia lam
674	76	6.4	474	2	Q3MEJ3_ANAVT	anabaena va
675	76	6.4	484	2	Q9L227_ARATH	arabidopsis
676	76	6.4	487	2	Q6IVM6_9GAMM	uncultured
677	76	6.4	519	2	Q6CKO4_KLULA	kluyveromyc
678	76	6.4	567	2	Q7NBN0_MYCGA	mycoplasma
679	76	6.4	616	2	Q52S70_ORYSA	oryza sativ
680	76	6.4	648	2	Q7PVU9_ANOGA	anopheles g
681	76	6.4	669	2	Q3XSP4_9PROT	magnetococc
682	76	6.4	699	2	DHX9_CAEEL	caenorhabdi
683	76	6.4	851	2		
684	76	6.4	931	2		
685	76	6.4	931	2		
686	76	6.4	953	2		
687	76	6.4	1297	2		
688	76	6.4	1301	1		

No.	%	pI	Len	N	Accession	ID / Organism
689	76	6.4	1409	2	Q4DU29_TRYCR	Q4du29 trypanosoma
690	76	6.4	1480	1	CFTR_RABIT	Q00554 oryctolagus
691	76	6.4	1551	1	Q96WN_VENIN	Q96wn venturia in
692	76	6.4	1783	2	Q18698_CAEEL	Q18698 caenorhabdi
693	76	6.4	1877	2	Q8MQA1_CAEEL	Q8mqa1 caenorhabdi
694	76	6.4	2009	2	Q7R8P2_PLAYO	Q7r8p2 plasmodium
695	76	6.4	3010	2	P90191_9HEPC	P90191 hepatitis c
696	76	6.4	3010	2	P90193_9HEPC	P90193 hepatitis c
697	76	6.4	3010	2	P90194_9HEPC	P90194 hepatitis c
698	75.5	6.3	156	1	MTR1A_RAT	P49218 rattus norv
699	75.5	6.3	162	2	Q66PG7_XENLA	Q66pg7 xenopus lae
700	75.5	6.3	203	2	Q2XP33_BACSU	Q2xp33 bacillus su
701	75.5	6.3	206	2	Q61TR8_CAEBR	Q61tr8 caenorhabdi
702	75.5	6.3	220	2	Q633A3_BACCZ	Q633a3 bacillus ce
703	75.5	6.3	228	2	Q9VUN8_DROME	Q9vun8 drosophila
704	75.5	6.3	231	2	Q6MD11_PARUW	Q6md11 parachlamyd
705	75.5	6.3	244	2	Q6B927_GRATL	Q6b927 gracilaria
706	75.5	6.3	247	2	Q7TPI3_RAT	Q7tpi3 rattus norv
707	75.5	6.3	248	2	Q63EZ9_BACCZ	Q63ez9 bacillus ce
708	75.5	6.3	248	2	Q6HMF5_BACHK	Q6hmf5 bacillus th
709	75.5	6.3	263	2	Q63GB2_BACCZ	Q63gb2 bacillus ce
710	75.5	6.3	263	2	Q6HNS6_BACHK	Q6hns6 bacillus th
711	75.5	6.3	263	2	Q81YU8_BACAN	Q81yu8 bacillus an
712	75.5	6.3	263	2	Q8CYF4_STRR6	Q8cyf4 streptococc
713	75.5	6.3	263	2	Q97PD2_STRPN	Q97pd2 streptococc
714	75.5	6.3	266	2	Q5IPF7_9RODE	Q5ipf7 perognathus
715	75.5	6.3	269	2	Q66PG6_XENLA	Q66pg6 xenopus lae
716	75.5	6.3	278	2	Q865K7_MACEU	Q865k7 macropus eu
717	75.5	6.3	279	2	Q3BSJ4_XANC5	Q3bsj4 xanthomonas
718	75.5	6.3	282	2	Q3A9G4_CARHZ	Q3a9g4 carboxydoth
719	75.5	6.3	303	2	Q9KZ08_STRCO	Q9kz08 streptomyce
720	75.5	6.3	305	2	Q4S7P1_TETNG	Q4s7p1 tetraodon n
721	75.5	6.3	309	2	Q5C281_SCHJA	Q5c281 schistosoma
722	75.5	6.3	326	2	Q9ESJ3_RAT	Q9esj3 rattus norv
723	75.5	6.3	339	2	Q9KSB3_VIBCH	Q9ksb3 vibrio chol
724	75.5	6.3	342	2	Q59TA5_CANAL	Q59ta5 candida alb
725	75.5	6.3	342	2	Q9QEV3_HHV8	Q9qev3 human herpe
726	75.5	6.3	352	1	RNFD_ECOS7	P58325 escherichia
727	75.5	6.3	352	1	RNFD_ECOLI	P76182 escherichia
728	75.5	6.3	352	2	Q32OY7_SHIBS	Q32oy7 shigella bo
729	75.5	6.3	352	2	Q32FE3_SHIDS	Q32fe3 shigella dy
730	75.5	6.3	352	2	Q3Z1Y5_SHISS	Q3z1y5 shigella so
731	75.5	6.3	352	2	Q2MB69_ECOLI	Q2mb69 escherichia
732	75.5	6.3	352	2	Q8FH94_ECOL6	Q8fh94 escherichia
733	75.5	6.3	364	2	Q83KY5_SHIFL	Q83ky5 shigella fl
734	75.5	6.3	369	2	Q2ULL9_ASPOR	Q2ull9 aspergillus
735	75.5	6.3	371	2	Q3C185_THEET	Q3c185 thermoanaer
736	75.5	6.3	377	1	Q4R2L1_VARHI	Q4r2l1 varigula hil
737	75.5	6.3	377	2	Q2USP9_ASPOR	Q2usp9 aspergillus
738	75.5	6.3	379	1	CYB_ZAPTR	P23173 zapus trino
739	75.5	6.3	379	2	Q50BJ8_PERFA	Q50bj8 perognathus
740	75.5	6.3	389	2	Q8AYS5_HYLJA	Q8ays5 hyla japoni
741	75.5	6.3	397	2	Q9N4R5_CAEEL	Q9n4r5 caenorhabdi
742	75.5	6.3	397	2	Q6RXC2_HCMV	Q6rxc2 human cytom
743	75.5	6.3	400	2	Q4ZIY5_PLABE	Q4ziy5 plasmodium
744	75.5	6.3	401	2	Q3SSF2_NITWN	Q3ssf2 nitrobacter
745	75.5	6.3	410	2	Q70NW4_9BILA	Q70nw4 strongyloid
746	75.5	6.3	413	2	Q5UET7_ECOLI	Q5uet7 escherichia
747	75.5	6.3	415	1	TNAB_ECOS7	P23173 escherichia
748	75.5	6.3	415	1	TNAB_ECOLI	P23173 escherichia
749	75.5	6.3	415	2	Q5UEU4_ECOLI	Q5ueu4 escherichia
750	75.5	6.3	415	2	Q31UW3_SHIBS	Q31uw3 shigella bo
751	75.5	6.3	415	2	Q8FBV1_ECOL6	Q8fbv1 escherichia
752	75.5	6.3	417	2	Q2VTE8_APLCA	Q2vte8 aplysia cal
753	75.5	6.3	421	2	Q2P2G3_XANOR	Q2p2g3 xanthomonas
754	75.5	6.3	430	2	Q5X337_LEGPA	Q5x337 legionella
755	75.5	6.3	433	2	Q6FCC9_CAEEL	Q6fcc9 caenorhabdi
756	75.5	6.3	446	2	Q7S8U0_NEUCR	Q7s8u0 neurospora
757	75.5	6.3	466	2	Q4Y729_PLACH	Q4y729 plasmodium
758	75.5	6.3	471	1	5HT2A_MOUSE	P35363 mus musculu
759	75.5	6.3	471	2	Q54304_MOUSE	Q54304 mus musculu
760	75.5	6.3	481	2	Q8C0K0_MOUSE	Q8c0k0 mus musculu
761	75.5	6.3	482	2	Q9P6J0_SCHPO	Q9p6j0 schizosacch
762	75.5	6.3	491	2	Q6SWJ1_HCMV	Q6swj1 human cytom
763	75.5	6.3	491	2	Q6SWS4_HCMV	Q6sws4 human cytom
764	75.5	6.3	491	2	Q6SWV2_HCMV	Q6swv2 human cytom
765	75.5	6.3	491	2	Q6SWY1_HCMV	Q6swy1 human cytom
766	75.5	6.3	498	2	Q47543_CHLEU	Q47543 chlamydomon
767	75.5	6.3	501	2	Q6CH25_YARLI	Q6ch25 yarrowia li
768	75.5	6.3	521	2	Q40JQ8_EHRCH	Q40jq8 ehrlichia c
769	75.5	6.3	539	2	Q5CI52_CRYHO	Q5ci52 cryptospori
770	75.5	6.3	551	1	FLVC2_MOUSE	Q91x85 mus musculu
771	75.5	6.3	574	2	Q2Z9L7_9GAMM	Q2z9l7 shewanella
772	75.5	6.3	574	2	Q2Z917_9GAMM	Q2z917 shewanella
773	75.5	6.3	593	2	Q25322_HELPY	Q25322 helicobacte
774	75.5	6.3	646	2	Q5ZLM5_CHICK	Q5zlm5 gallus gall
775	75.5	6.3	708	2	Q22806_CAEEL	Q22806 caenorhabdi
776	75.5	6.3	746	2	Q8PGM4_XANAC	Q8pgm4 xanthomonas
777	75.5	6.3	773	1	CLCA_ARATH	Q96325 arabidopsis
778	75.5	6.3	773	2	P92941_ARATH	P92941 arabidopsis
779	75.5	6.3	795	2	Q61FI6_CAEBR	Q61fi6 caenorhabdi
780	75.5	6.3	939	2	Q5BG34_EMENI	Q5bg34 aspergillus
781	75.5	6.3	1008	2	Q89154_9HEPC	Q89154 hepatitis c
782	75.5	6.3	1010	2	Q3HAL4_TRIER	Q3hal4 trichodesmi
783	75.5	6.3	1088	2	Q4UI92_THEAN	Q4ui92 theileria a
784	75.5	6.3	1142	2	Q9UT41_SCHPO	Q9ut41 schizosacch
785	75.5	6.3	1583	2	Q7P9S4_RICSI	Q7p9s4 rickettsia
786	75.5	6.3	3010	2	Q9J3G7_9HEPC	Q9j3g7 hepatitis c
787	75	6.3	105	2	Q5AM04_CANAL	Q5am04 candida alb
788	75	6.3	132	2	Q6N505_RHOPA	Q6n505 rhodopseudo
789	75	6.3	152	2	Q2N8U7_9SPHN	Q2n8u7 erythrobact
790	75	6.3	156	2	Q81498_9HEPC	Q81498 hepatitis c
791	75	6.3	156	2	Q81507_9HEPC	Q81507 hepatitis c
792	75	6.3	156	2	Q81531_9HEPC	Q81531 hepatitis c
793	75	6.3	170	2	Y1368_METJA	Y1368 methanococc
794	75	6.3	194	2	Q63IU3_BACCZ	Q63iu3 bacillus ce
795	75	6.3	202	2	Q3J4F0_RHOS4	Q3j4f0 rhodobacter
796	75	6.3	215	2	Q36M19_MARHY	Q36m19 marinobacte
797	75	6.3	215	2	Q34238_CAPSU	Q34238 capricornis
798	75	6.3	218	2	Q336X2_ORYSA	Q336x2 oryza sativ
799	75	6.3	220	2	Q4I989_ARTAU	Q4i989 arthrobacte
800	75	6.3	220	2	Q6SKB1_ARTAU	Q6skb1 staphylococ
801	75	6.3	225	2	Q5FF13_EHRRG	Q5ff13 ehrlichia r
802	75	6.3	225	2	Q6VMD0_9CORO	Q6vmd0 ochrona hy
803	75	6.3	227	2	Q9GAT3_9CORO	Q9gat3 ralstonia m
804	75	6.3	227	2	Q3RXW8_RALME	Q3rxw8 thermoanaer
805	75	6.3	228	2	Q4YQG6_PLABE	Q4yqg6 plasmodium
806	75	6.3	232	2	Q3CFK0_THEET	Q3cfk0 methanococc
807	75	6.3	249	1	Y1368_METJA	Q58763 methanosarc
808	75	6.3	256	2	Q631U3_BACCZ	Q631u3 bacillus ce
809	75	6.3	273	2	Q3VLP9_9CHLB	Q3vlp9 pelodictyon
810	75	6.3	274	2	Q9KNDO_VIBCH	Q9kndo vibrio chol
811	75	6.3	277	2	Q6MN43_BDEBA	Q6mn43 bdellovibri
812	75	6.3	280	2	Q44K03_CHRSL	Q44k03 chromobacte
813	75	6.3	294	2	Q8RET4_FUSNN	Q8ret4 fusobacteri
814	75	6.3	302	2	Q6CVK2_KLULA	Q6cvk2 kluyveromyc
815	75	6.3	311	2	Q5ZLG8_CHICK	Q5zlg8 gallus gall
816	75	6.3	318	2	Q4SMC3_TETNG	Q4smc3 tetraodon n
817	75	6.3	330	2	Q58239_PYRHO	Q58239 pyrococcus
818	75	6.3	368	2	Q467V3_METBA	Q467v3 methanosarc
819	75	6.3	371	2	Q3TS71_MOUSE	Q3ts71 mus musculu
820	75	6.3	371	2	Q8BW45_MOUSE	Q8bw45 mus musculu
821	75	6.3	373	1	PE2R3_PIG	P50131 sus scrofa
822	75	6.3	375	2	Q48ME7_PSE14	Q48me7 pseudomonas
823	75	6.3	380	1	CYB_RANRU	Q69GZ7_9PERO	rana ruosa
824	75	6.3	387	2	Q69GJ2_9PERO	Q69gj2 nandus nebu
825	75	6.3	407	2	Q46657_PIG	Q46657 sus scrofa
826	75	6.3	418	2	Q7NRF5_CHRVO	Q7nrf5 chromobacte
827	75	6.3	418	2	Q6QFB8_LEGPN	Q6qfb8 legionella
828	75	6.3	418	2	Q6A8T1_PROAC	Q6a8t1 propionibac
829	75	6.3	418	2	Q5WZ83_LEGPL	Q5wz83 legionella
830	75	6.3	424	2	Q5X7T2_LEGPA	Q5x7t2 legionella
831	75	6.3	425	2	Q2N984_9SPHN	Q2n984 erythrobact
832	75	6.3	460	2	Q4Z7S9_PLABE	Q4z7s9 plasmodium
833	75	6.3	460	2	Q3JN15_BURP1	Q3jn15 burkholderi
834	75	6.3	460	2	Q62GF6_BURMA	Q62gf6 burkholderi

#					Entry	Accession	Species
835	75	6.3	460	2	Q63QA3_BURPS	q63qa3	burkholderi
836	75	6.3	473	1	GBRR1_HUMAN	P24046	homo sapien
837	75	6.3	473	2	Q9BX06_HUMAN	q9bx06	homo sapien
838	75	6.3	476	2	Q46N18_RALEJ	q46n18	ralstonia e
839	75	6.3	488	2	Q7RW58_NEURO	q7rw58	neurospora
840	75	6.3	498	2	Q7U567_FUGRU	q7u567	fugu rubrip
841	75	6.3	526	2	Q9SN21_ARATH	q9sn21	arabidopsis
842	75	6.3	543	2	Q7NS50_CHRVO	q7ns50	chromobacte
843	75	6.3	625	1	KUP2_LEGPH	q5ztn5	legionella
844	75	6.3	649	2	O34952_BACSU	o34952	bacillus su
845	75	6.3	662	2	Q7VED4_PROMA	q7ved4	prochlorococ
846	75	6.3	753	2	Q98S90_GUITH	q98s90	guillardia
847	75	6.3	761	2	Q3GE97_9FIRM	q3ge97	syntrophomo
848	75	6.3	777	2	Q6BG55_PARTE	q6bg55	paramecium
849	75	6.3	834	2	Q2I6B0_RAT	q2i6b0	rattus norv
850	75	6.3	838	2	Q4HZA9_GIB2E	q4hza9	gibberella
851	75	6.3	883	2	Q4N4I2_THEPA	q4n4i2	theileria p
852	75	6.3	885	2	Q8PU16_METMA	q8pu16	methanosarc
853	75	6.3	937	2	Q82ZR7_ENTFA	q82zr7	enterococcu
854	75	6.3	1008	2	O89152_9HEPC	o89152	hepatitis c
855	75	6.3	1008	2	O89153_9HEPC	o89153	hepatitis c
856	75	6.3	1008	2	O89156_9HEPC	o89156	hepatitis c
857	75	6.3	1131	2	Q8NAT5_HUMAN	q8nat5	homo sapien
858	75	6.3	1145	1	Q8GUE7_9LILI	q8gue7	cymodocea n
859	75	6.3	1146	2	Q31LG0_PSEHT	q31lg0	pseudoalter
860	75	6.3	1154	2	Q6FTG6_CANGA	q6ftg6	candida gla
861	75	6.3	1336	2	Q6F1J1_MESFL	q6f1j1	mesoplasma
862	75	6.3	1703	2	Q38B01_9TRYP	q38b01	trypanosoma
863	75	6.3	1704	2	Q95206_9TRYP	q95206	trypanosoma
864	75	6.3	3010	2	Q9QIY7_9HEPC	q9qiy7	hepatitis c
865	75	6.3	2248	1	CYA1_DROME	q9qiy8	drosophila
866	75	6.3	2846	2	Q55EL4_DICDI	q55el4	dictyosteli
867	75	6.3	3010	2	Q68833_9HEPC	q68833	hepatitis c
868	75	6.3	3010	2	Q9J3G2_9HEPC	q9j3g2	hepatitis c
869	75	6.3	3010	2	Q9J3G5_9HEPC	q9j3g5	hepatitis c
870	75	6.3	3010	2	Q9QIY8_9HEPC	q9qiy8	hepatitis c
871	74.5	6.2	159	2	Q34A83_RHOPA	q34a83	rhodopseudo
872	74.5	6.2	174	2	P97068_9ENTR	p97068	salmonella
873	74.5	6.2	179	2	Q8EPH9_OCEIH	q8eph9	oceanobacil
874	74.5	6.2	180	2	P71253_ECOLI	p71253	escherichia
875	74.5	6.2	222	2	Q32DT0_SHIDS	q32dt0	shigella dy
876	74.5	6.2	227	2	Q9GAT4_OCHCU	q9gat4	ochotona cu
877	74.5	6.2	227	2	Q9GAT5_OCHTI	q9gat5	ochotona th
878	74.5	6.2	227	2	Q9GAT6_OCHPR	q9gat6	ochotona pr
879	74.5	6.2	258	2	Q88WC7_LACPL	q88wc7	lactobacill
880	74.5	6.2	276	2	Q9R905_RHIME	q9r905	rhizobium m
881	74.5	6.2	278	2	Q2R1I5_ORYSA	q2r1i5	oryza sativ
882	74.5	6.2	280	2	Q6WIF6_SYNP8	q6wif6	synechococc
883	74.5	6.2	290	2	Q6SEU1_9BACT	q6seu1	uncultured
884	74.5	6.2	294	2	Q4CJI1_CLOTM	q4cji1	clostridium
885	74.5	6.2	298	2	Q6BWD3_DEBHA	q6bwd3	debaryomyce
886	74.5	6.2	298	2	Q5IEN3_ENTHI	q5ien3	entamoeba h
887	74.5	6.2	313	2	Q8R7X6_THETN	q8r7x6	thermoanaer
888	74.5	6.2	335	2	Q9WXS7_THEMA	q9wxs7	thermotoga
889	74.5	6.2	346	2	Q5FMX7_LACAC	q5fmx7	lactobacill
890	74.5	6.2	355	1	CX3C1_HUMAN	q9wxs7	homo sapien
891	74.5	6.2	358	2	Q5WHN9_BACSK	q5whn9	bacillus cl
892	74.5	6.2	363	2	Q48VQ7_STRPM	q48vq7	streptococc
893	74.5	6.2	364	2	Q8IDY2_PLAF7	q8idy2	plasmodium
894	74.5	6.2	377	2	Q4R1V2_VARHI	q4r1v2	vargula hil
895	74.5	6.2	377	2	Q4R1V3_VARHI	q4r1v3	vargula hil
896	74.5	6.2	377	2	Q4R1V6_VARHI	q4r1v6	vargula hil
897	74.5	6.2	377	2	Q4R1W3_VARHI	q4r1w3	vargula hil
898	74.5	6.2	377	2	Q4R1X3_VARHI	q4r1x3	vargula hil
899	74.5	6.2	377	2	Q4R1Y1_VARHI	q4r1y1	vargula hil
900	74.5	6.2	377	2	Q4R1Y8_VARHI	q4r1y8	vargula hil
901	74.5	6.2	377	2	Q4R1Z4_VARHI	q4r1z4	vargula hil
902	74.5	6.2	377	2	Q4R126_VARHI	q4r126	vargula hil
903	74.5	6.2	377	2	Q4R128_VARHI	q4r128	vargula hil
904	74.5	6.2	377	2	Q4R201_VARHI	q4r201	vargula hil
905	74.5	6.2	377	2	Q4R222_VARHI	q4r222	vargula hil
906	74.5	6.2	377	2	Q4R223_VARHI	q4r223	vargula hil
907	74.5	6.2	377	2	Q4R244_VARHI	q4r244	vargula hil
908	74.5	6.2	377	2	Q4R254_VARHI	q4r254	vargula hil
909	74.5	6.2	377	2	Q4R268_VARHI	q4r268	vargula hil
910	74.5	6.2	377	2	Q4R273_VARHI	q4r273	vargula hil
911	74.5	6.2	377	2	Q4R285_VARHI	q4r285	vargula hil
912	74.5	6.2	377	2	Q4R286_VARHI	q4r286	vargula hil
913	74.5	6.2	377	2	Q4R288_VARHI	q4r288	vargula hil
914	74.5	6.2	377	2	Q4R289_VARHI	q4r289	vargula hil
915	74.5	6.2	377	2	Q4R290_VARHI	q4r290	vargula hil
916	74.5	6.2	377	2	Q4R292_VARHI	q4r292	vargula hil
917	74.5	6.2	377	2	Q4R294_VARHI	q4r294	vargula hil
918	74.5	6.2	377	2	Q4R295_VARHI	q4r295	vargula hil
919	74.5	6.2	377	2	Q4R296_VARHI	q4r296	vargula hil
920	74.5	6.2	377	2	Q4R299_VARHI	q4r299	vargula hil
921	74.5	6.2	377	2	Q4R2A2_VARHI	q4r2a2	vargula hil
922	74.5	6.2	377	2	Q4R2A9_VARHI	q4r2a9	vargula hil
923	74.5	6.2	377	2	Q4R2B4_VARHI	q4r2b4	vargula hil
924	74.5	6.2	377	2	Q4R2C4_VARHI	q4r2c4	vargula hil
925	74.5	6.2	377	2	Q4R2C9_VARHI	q4r2c9	vargula hil
926	74.5	6.2	377	2	Q4R2D6_VARHI	q4r2d6	vargula hil
927	74.5	6.2	377	2	Q4R2E3_VARHI	q4r2e3	vargula hil
928	74.5	6.2	377	2	Q4R2E4_VARHI	q4r2e4	vargula hil
929	74.5	6.2	377	2	Q4R2E7_VARHI	q4r2e7	vargula hil
930	74.5	6.2	377	2	Q4R2F7_VARHI	q4r2f7	vargula hil
931	74.5	6.2	377	2	Q4R2G0_VARHI	q4r2g0	vargula hil
932	74.5	6.2	377	2	Q4R2G6_VARHI	q4r2g6	vargula hil
933	74.5	6.2	377	2	Q4R2H6_VARHI	q4r2h6	vargula hil
934	74.5	6.2	377	2	Q4R2H9_VARHI	q4r2h9	vargula hil
935	74.5	6.2	377	2	Q4R2I1_VARHI	q4r2i1	vargula hil
936	74.5	6.2	377	2	Q4R2J3_VARHI	q4r2j3	vargula hil
937	74.5	6.2	377	2	Q4R2K1_VARHI	q4r2k1	vargula hil
938	74.5	6.2	377	2	Q4R2K2_VARHI	q4r2k2	vargula hil
939	74.5	6.2	377	2	Q4R2K3_VARHI	q4r2k3	vargula hil
940	74.5	6.2	377	2	Q4R2K5_VARHI	q4r2k5	vargula hil
941	74.5	6.2	377	2	Q4R2K8_VARHI	q4r2k8	vargula hil
942	74.5	6.2	377	2	Q4R2M1_VARHI	q4r2m1	vargula hil
943	74.5	6.2	377	2	Q4R2M8_VARHI	q4r2m8	vargula hil
944	74.5	6.2	377	2	Q4R2N2_VARHI	q4r2n2	vargula hil
945	74.5	6.2	377	2	Q4R2N4_VARHI	q4r2n4	vargula hil
946	74.5	6.2	377	2	Q4R2N5_VARHI	q4r2n5	vargula hil
947	74.5	6.2	377	2	Q4R2N6_VARHI	q4r2n6	vargula hil
948	74.5	6.2	377	2	Q4R2P2_VARHI	q4r2p2	vargula hil
949	74.5	6.2	377	2	Q4R2P4_VARHI	q4r2p4	vargula hil
950	74.5	6.2	377	2	Q4A6X7_MYCS5	q4a6x7	mycoplasma
951	74.5	6.2	378	2	Q6DUV8_BRANA	q6duv8	brassica na
952	74.5	6.2	379	2	Q9GBZ4_OCHPR	q9gbz4	ochotona pr
953	74.5	6.2	379	2	Q9SY2_CANAL	q9sy2	candida alb
954	74.5	6.2	379	2	Q65MD8_BACLD	q65md8	bacillus li
955	74.5	6.2	379	1	ALG10_CANAL	alg10	candida alb
956	74.5	6.2	379	1	CYB_OCHPR	cyb	ochotona pr
957	74.5	6.2	392	1	5HT2A_RAT	p14842	rattus norv
958	74.5	6.2	415	2	P14842_RAT	p14842	rattus norv
959	74.5	6.2	442	2	Q4U3W9_MESAU	q4u3w9	mesocricetu
960	74.5	6.2	450	2	Q9K5Y9_BACHD	q9k5y9	bacillus ha
961	74.5	6.2	458	2	Q6QU71_ASPFU	q6qu71	aspergillus
962	74.5	6.2	471	2	O24348_SORBI	o24348	sorghum bic
963	74.5	6.2	471	2	Q2RU28_RHORU	q2ru28	rhodospiril
964	74.5	6.2	471	2	Q55UE4_CRYNE	q55ue4	cryptococcu
965	74.5	6.2	473	2	Q5K102_CRYNE	q5k102	cryptococcu
966	74.5	6.2	488	2	Q66GG5_ARATH	q66gg5	arabidopsis
967	74.5	6.2	500	2	Q8N2B3_HUMAN	q8n2b3	homo sapien
968	74.5	6.2	510	2	Q22454_WHEAT	q22454	wheat
969	74.5	6.2	523	2	Q4WLQ1_ASPFU	q4wlq1	aspergillus
970	74.5	6.2	523	2	Q9VD40_DROME	q9vd40	drosophila
971	74.5	6.2	540	2	Q31EZ1_PSEHT	q31ez1	pseudoalter
972	74.5	6.2	562	1	YKR4_YEAST	p36029	saccharomyc
973	74.5	6.2	594	2	P36029_PSEHT	p36029	pseudoalter
974	74.5	6.2	615	2	Q2X3C4_9GAMM	q2x3c4	shewanella
975	74.5	6.2	618	2	Q2ZVR1_SHEPU	q2zvr1	shewanella
976	74.5	6.2	620	2	Q36IN8_9GAMM	q36in8	shewanella
977	74.5	6.2	620	2	Q2ZVR1_SHEPU	q2zvr1	shewanella
978	74.5	6.2	620	2	Q36IN8_9GAMM	q36in8	shewanella
979	74.5	6.2	793	2	Q4PCY9_USTMA	q4pcy9	ustilago ma
980	74.5	6.2	848	2	Q8VVK9_CORGL	q8vvk9	corynebacte

No	Score	E	Len	N	Code	Accession	Organism
981	74.5	6.2	990	1	FTSK_VIBVU	Q8dbm2	vibrio vuln
982	74.5	6.2	1004	2	Q3H520_9ACTO	Q3h520	nocardioide
983	74.5	6.2	1022	2	Q4U8N7_THEAN	Q4u8n7	theileria a
984	74.5	6.2	1023	2	Q38FL3_9TRYP	Q38fl3	trypanosoma
985	74.5	6.2	1033	2	Q382A3_9TRYP	Q382a3	trypanosoma
986	74.5	6.2	1034	2	Q72ZC1_TRYBB	Q72zc1	trypanosoma
987	74.5	6.2	1034	2	Q72ZC0_9TRYP	Q72zc0	trypanosoma
988	74.5	6.2	1183	2	Q94447_CALVI	Q94447	calliphora
989	74.5	6.2	1401	2	Q61PW5_CAEBR	Q61pw5	caenorhabdi
990	74.5	6.2	1520	2	Q8T687_DICDI	Q8t687	dictyosteli
991	74.5	6.2	1534	2	Q54TV1_DICDI	Q54tv1	dictyosteli
992	74.5	6.2	1559	2	Q7S0S1_NEUCR	Q7s0s1	neurospora
993	74.5	6.2	1640	2	Q54ZZ5_DICDI	Q54zz5	dictyosteli
994	74.5	6.2	1808	2	Q9LYS6_ARATH	Q9lys6	arabidopsis
995	74.5	6.2	1837	2	Q8IKF1_PLAF7	Q8ikf1	plasmodium
996	74.5	6.2	3010	2	Q91AU0_9HEPC	Q91au0	hepatitis c
997	74.5	6.2	124	2	Q31RW0_CHLTE	Q31rw0	chlorobium
998	74.5	6.2	156	2	Q8KC46_9HEPC	Q8kc46	hepatitis c
999	74	6.2	167	2	Q81S28_HUMAN	Q81s28	homo sapien
1000	74	6.2	173	2	Q8WZ72_HUMAN	Q8wz72	homo sapien
1001	74	6.2	193	2	Q5VHX0_EAV	Q5vhx0	equine arte
1002	74	6.2	220	2	Q5HCD2_EHRRW	Q5hcd2	ehrlichia r
1003	74	6.2	225	2	Q91SA2_9CORO	Q91sa2	coronavirus
1004	74	6.2	230	2	Q8BY70_LACPL	Q8by70	lactobacill
1005	74	6.2	231	1	COBS2_ARCFU	O27961	archaeoglob
1006	74	6.2	231	2	O28892_ARCFU	O28892	archaeoglob
1007	74	6.2	238	2	Q6HET1_BACHK	Q6het1	bacillus th
1008	74	6.2	249	2	Q36H4_9GAMM	Q36h4	shewanella
1009	74	6.2	255	2	Q66483_EAV	Q66483	equine arte
1010	74	6.2	262	2	Q31RW0_SYNP7	Q31rw0	synechococc
1011	74	6.2	278	2	Q6CU18_KLULA	Q6cu18	kluyveromyc
1012	74	6.2	279	2	Q4XPR5_PLACH	Q4xpr5	plasmodium
1013	74	6.2	285	2	Q4E472_TRYCR	Q4e472	trypanosoma
1014	74	6.2	286	1	POTB_MYCPN	P75058	mycoplasma
1015	74	6.2	291	2	Q4AVT5_9BURK	Q4avt5	polaromonas
1016	74	6.2	291	2	Q66G98_YERPS	Q66g98	yersinia ps
1017	74	6.2	295	1	CYOE_PSEPU	Q9wwr5	pseudomonas
1018	74	6.2	295	2	Q6N4M3_PSEPU	Q6n4m3	pseudomonas
1019	74	6.2	295	2	Q416Y2_KINRA	Q416y2	kineococcus
1020	74	6.2	297	2	Q61BC3_CAEBR	Q61bc3	caenorhabdi
1021	74	6.2	300	1	NU2M_ASCSU	P24877	ascaris suu
1022	74	6.2	309	2	Q3DPI9_STRAG	Q3dpi9	streptococc
1023	74	6.2	312	2	Q9YBD4_AERPE	Q9ybd4	aeropyrum p
1024	74	6.2	312	2	Q9CH74_LACLA	Q9ch74	lactococcus
1025	74	6.2	315	2	Q71O92_SPAEH	Q71o92	spalax leuc
1026	74	6.2	321	2	Q8M6V0_9MAXI	Q8m6v0	tigriopus j
1027	74	6.2	324	2	Q8DVZ6_STRMU	Q8dvz6	streptococc
1028	74	6.2	330	2	Q3TU35_MOUSE	Q3tu35	mus musculu
1029	74	6.2	331	2	Q3HOJ0_9ACTO	Q3hoj0	nocardioide
1030	74	6.2	333	2	Q4FN51_PELUB	Q4fn51	pelagibacte
1031	74	6.2	339	2	Q61FG9_CAEBR	Q61fg9	caenorhabdi
1032	74	6.2	342	2	Q621V1_CAEBR	Q621v1	caenorhabdi
1033	74	6.2	349	1	I10R2_MOUSE	Q61190	mus musculu
1034	74	6.2	350	1	MTR1A_HUMAN	P48039	homo sapien
1035	74	6.2	351	2	Q8VHM7_MOUSE	Q8vhm7	mus musculu
1036	74	6.2	354	2	Q6SU34_MANSM	Q6su34	mannheimia
1037	74	6.2	357	2	Q5FVV6_MEDTR	Q5fvv6	medicago tr
1038	74	6.2	359	2	Q3ITR5_NATPD	Q3itr5	natronomona
1039	74	6.2	361	2	Q64AL9_9ARCH	Q64al9	uncultured
1040	74	6.2	372	2	Q4CMV5_TRYCR	Q4cmv5	trypanosoma
1041	74	6.2	379	1	CYB_THOMO	Q8wek2	thomomys mo
1042	74	6.2	379	2	Q47980_THOBO	Q47980	thomomys bo
1043	74	6.2	379	2	Q48002_THOMO	Q48002	thomomys mo
1044	74	6.2	379	2	Q48003_THOMO	Q48003	thomomys mo
1045	74	6.2	379	2	Q59JJ7_9SCIU	Q59jj7	pteromys vo
1046	74	6.2	379	2	Q8HHJ7_THOBO	Q8hhj7	thomomys bo
1047	74	6.2	380	2	Q8WEK5_THOTA	Q8wek5	thomomys ta
1048	74	6.2	381	1	CYB_PSENI	Q74kb0	pseudantech
1049	74	6.2	381	2	Q35553_LACCO	Q35553	lactobacill
1050	74	6.2	382	2	Q5R7A1_PONPY	Q5r7a1	pongo pygma
1051	74	6.2	396	2	Q2YWW7_STAAB	Q2yww7	staphylococ
1052	74	6.2	396	2	Q6GAR1_STAAS	Q6gar1	staphylococ
1053	74	6.2	396	2	Q6GI68_STAAR	Q6gi68	staphylococ
1054	74	6.2	396	2	Q7A6D3_STAAN	Q7a6d3	staphylococ
1055	74	6.2	396	2	Q8NXC4_STAAW	Q8nxc4	staphylococ
1056	74	6.2	396	2	Q99V76_STAAM	Q99v76	staphylococ
1057	74	6.2	396	2	Q5HH70_STAAC	Q5hh70	staphylococ
1058	74	6.2	397	2	Q42254_PLABE	Q42254	plasmodium
1059	74	6.2	398	2	Q2PQV8_9NOCA	Q2pqv8	rhodococcus
1060	74	6.2	398	2	Q5NEU8_FRATT	Q5neu8	francisella
1061	74	6.2	406	2	Q3FR83_9BURK	Q3fr83	burkholderi
1062	74	6.2	410	2	Q4RIO3_TETNG	Q4rio3	tetraodon n
1063	74	6.2	418	2	Q6QFB9_LEGPN	Q6qfb9	legionella
1064	74	6.2	418	2	Q6QCS5_LEGPN	Q6qcs5	legionella
1065	74	6.2	418	2	Q6QFC7_LEGPN	Q6qfc7	legionella
1066	74	6.2	436	2	Q5QZG8_IDILO	Q5qzg8	idiomarina
1067	74	6.2	442	2	Q9CEG6_LACLA	Q9ceg6	lactococcus
1068	74	6.2	452	2	Q2S5B2_9GAMM	Q2s5b2	shewanella
1069	74	6.2	452	2	Q4NJC7_9MICC	Q4njc7	arthrobacte
1070	74	6.2	457	2	Q8RBZ7_THETN	Q8rbz7	thermoanaer
1071	74	6.2	459	2	Q39U36_GEOMG	Q39u36	geobacter m
1072	74	6.2	475	2	Q9S2G7_STRCO	Q9s2g7	streptomyce
1073	73.5	6.2	481	2	Q4Q1F4_LEIMA	Q4q1f4	leishmania
1074	73.5	6.2	485	2	Q9XVK0_CAEEL	Q9xvk0	caenorhabdi
1075	73.5	6.2	487	2	O23384_ARATH	O23384	arabidopsis
1076	73.5	6.2	493	2	Q9EVJ7_FLABU	Q9evj7	flavobacter
1077	73.5	6.2	503	2	Q6M052_METMP	Q6m052	methanococc
1078	73.5	6.2	505	2	Q2IKZ1_9DELT	Q2ikz1	anaeromyxob
1079	73.5	6.2	528	2	Q70LQ9_KLULA	Q70lq9	kluyveromyc
1080	73.5	6.2	530	2	Q41SGO_FERAC	Q41sgo	ferroplasma
1081	73.5	6.2	530	2	Q51FL8_ENTHI	Q51fl8	entamoeba h
1082	73.5	6.2	540	2	Q6LF33_PLAF7	Q6lf33	plasmodium
1083	73.5	6.2	581	2	Q6FII6_CANGA	Q6fii6	candida gla
1084	73.5	6.2	584	2	Q5KA08_CRYNE	Q5ka08	kluyveromyc
1085	73.5	6.2	587	2	Q43QW4_SOLUS	Q43qw4	novosphingo
1086	73.5	6.2	599	2	Q5KA09_CRYNE	Q5ka09	candida gla
1087	73.5	6.2	650	2	Q9S6S6_9LACT	Q9s6s6	carsonella
1088	73.5	6.2	681	2	Q4FTS7_PSYAR	Q4fts7	lactococcus
1089	73.5	6.2	689	2	Q37RQ8_SPHAR	Q37rq8	psychrobact
1090	73.5	6.2	742	2	Q6FNV6_CANGA	Q6fnv6	novosphingo
1091	73.5	6.2	841	2	Q9AIP1_CARRU	Q9aip1	candida gla
1092	73.5	6.2	846	2	Q93U47_CARRU	Q93u47	carsonella
1093	73.5	6.2	892	2	Q8TGB2_CANAL	Q8tgb2	carsonella
1094	73.5	6.2	943	2	Q4IMI9_GIBZE	Q4imi9	candida alb
1095	73.5	6.2	1123	2	Q9SE99_ARATH	Q9se99	gibberella
1096	73.5	6.2	1123	2	Q9SPU7_ARATH	Q9spu7	arabidopsis
1097	73.5	6.2	1123	2	Q9SIS2_ARATH	Q9sis2	arabidopsis
1098	73.5	6.2	1216	2	Q5KCX7_CRYNE	Q5kcx7	cryptococcu
1099	73.5	6.2	1216	2	Q913V3_9HEPC	Q913v3	cryptococcu
1100	73.5	6.2	3010	2	Q9DTE8_9HEPC	Q9dte8	hepatitis c
1101	73.5	6.2	3010	2	Q9J3H6_9HEPC	Q9j3h6	hepatitis c
1102	73.5	6.2	3010	2	Q9QIY1_9HEPC	Q9qiy1	hepatitis c
1103	73.5	6.2	3010	2	Q9QIY2_9HEPC	Q9qiy2	hepatitis c
1104	73.5	6.2	120	2	Q9SKA6_ARATH	Q9ska6	arabidopsis
1105	73.5	6.2	153	2	Q92XD3_RHIME	Q92xd3	rhizobium m
1106	73.5	6.2	174	2	Q2NGT7_9EURY	Q2ngt7	methanospha
1107	73.5	6.2	180	2	Q8ZXS3_PYRAE	Q8zxs3	pyrobaculum
1108	73.5	6.2	180	2	P71251_ECOLI	P71251	escherichia
1109	73.5	6.2	180	2	P71257_ECOLI	P71257	escherichia
1110	73.5	6.2	199	2	P75018_ECOLI	P75018	escherichia
1111	73.5	6.2	216	1	Y2O3_AQUAE	O67827	aquifex aeo
1112	73.5	6.2	217	2	Q4TEY9_TETNG	Q4tey9	tetraodon n
1113	73.5	6.2	226	2	Q5MAP0_9CORO	Q5map0	infectious
1114	73.5	6.2	226	2	Q9J0XI_9CORO	Q9j0xi	infectious
1115	73.5	6.2	246	2	Q4D4K9_TRYCR	Q4d4k9	trypanosoma
1116	73.5	6.2	246	2	Q50Z61_ENTHI	Q50z61	entamoeba h
1117	73.5	6.2	267	2	Q50Z62_ENTHI	Q50z62	entamoeba h
1118	73.5	6.2	270	2	Q8HBP0_PERLO	Q8hbp0	perognathus
1119	73.5	6.2	270	2	Q8HIY6_PERLO	Q8hiy6	perognathus
1120	73.5	6.2	274	2	Q95L51_CAPHI	Q95l51	capra hircu
1121	73.5	6.2	278	2	Q4JC08_SULAC	Q4jc08	sulfolobus
1122	73.5	6.2	281	2	Q3NN12_SHEFR	Q3nn12	shewanella
1123	73.5	6.2	281	2	Q2SQF4_9GAMM	Q2sqf4	shewanella
1124	73.5	6.2	281	2	Q4HSI6_CAMUP	Q4hsi6	hahella che
1125	73.5	6.2	298	2	Q6ZTT3_ORYSA	Q6ztt3	oryza sativ
1126	73.5	6.2	303	2	Q5J3K6_RAT	Q5j3k6	rattus norv

No.			Len	N	Accession	ID / Organism
1127	73.5	6.2	304	2	Q2RIE6_MOOTH	q2rie6 moorella th
1128	73.5	6.2	304	2	Q5NP42_ZYMMO	q5np42 zymomonas m
1129	73.5	6.2	305	2	Q4P0E6_USTMA	q4p0e6 ustilago ma
1130	73.5	6.2	306	2	Q37MI0_RHOPA	q37mi0 rhodopseudo
1131	73.5	6.2	307	2	Q2IYA5_RHOPA	q2iya5 rhodopseudo
1132	73.5	6.2	316	2	Q3AQX9_CHLCH	q3aqx9 chlorobium
1133	73.5	6.2	318	2	Q55895_SYNY3	q55895 synechocyst
1134	73.5	6.2	338	1	YTAD_BACSU	ytad bacillus su
1135	73.5	6.2	355	2	Q4J826_SULAC	q4j826 sulfolobus
1136	73.5	6.2	359	2	Q2NTQ3_SODGL	q2ntq3 sodalis glo
1137	73.5	6.2	360	2	Q8UUW8_BRARE	q8uuw8 brachydanio
1138	73.5	6.2	367	2	Q64BD6_9ARCH	q64bd6 uncultured
1139	73.5	6.2	373	2	Q5FI17_LACAC	q5fi17 lactobacill
1140	73.5	6.2	379	1	Q35457	q35457 phoca groen
1141	73.5	6.2	379	1	CYB_THOTA	cyb_thota thomomys ta
1142	73.5	6.2	379	2	CYB_PHOGR	cyb_phogr phoca groen
1143	73.5	6.2	379	2	OPGC_SALTI	opgc_salti salmonella
1144	73.5	6.2	379	2	Q9G3M8_OCHCU	q9g3m8 ochotona cu
1145	73.5	6.2	379	2	Q50BJ0_9RODE	q50bj0 perognathus
1146	73.5	6.2	380	1	Q50BJ7_PERPA	q50bj7 perognathus
1147	73.5	6.2	384	1	Q588N6_SCILI	q588n6 scirus lis
1148	73.5	6.2	385	2	Q588N8_SCILI	q588n8 scirus lis
1149	73.5	6.2	387	2	Q2N2B6_PERPA	q2n2b6 perognathus
1150	73.5	6.2	387	2	OXYR_MACMU	oxyr_macmu macaca mula
1151	73.5	6.2	389	2	OXYR_BOVIN	oxyr_bovin bos taurus
1152	73.5	6.2	391	2	Q7MVX5_PORGI	q7mvx5 porphyromon
1153	73.5	6.2	397	2	Q9KWU2_9SPHN	q9kwu2 sphingomona
1154	73.5	6.2	398	2	P94442_BACSU	p94442 bacillus su
1155	73.5	6.2	409	1	OPGZ7_ENTFA	opgz7 enterococcu
1156	73.5	6.2	413	2	Q3CNW3_ALTAI	q3cnw3 pseudoalter
1157	73.5	6.2	421	2	Q7V140_PROMP	q7v140 prochloroco
1158	73.5	6.2	425	2	Q92ST3_LISIN	q92st3 listeria in
1159	73.5	6.2	435	2	Q8PK37_XANAC	q8pk37 xanthomonas
1160	73.5	6.2	442	2	Q6D6K1_ERWCT	q6d6k1 erwinia car
1161	73.5	6.2	442	2	Q48IN0_COLP3	q48in0 colwellia p
1162	73.5	6.2	451	2	Q8GZ34_ARATH	q8gz34 arabidopsis
1163	73.5	6.2	451	2	Q8GZ34_ARATH	q8gz34 arabidopsis
1164	73.5	6.2	470	2	Q9XIQ7_ARATH	q9xiq7 arabidopsis
1165	73.5	6.2	491	1	Q4E247_TRYCR	q4e247 trypanosoma
1166	73.5	6.2	491	2	Q36Q01_MARHY	q36q01 marinobacte
1167	73.5	6.2	518	2	VIE1_HCMVA	vie1_hcmva human cytom
1168	73.5	6.2	523	2	P13202_HCMV	p13202 human cytom
1169	73.5	6.2	542	2	Q6SW28_HCMV	q6sw28 human cytom
1170	73.5	6.2	555	2	Q7RT44_PLAVO	q7rt44 plasmodium
1171	73.5	6.2	557	2	Q64WY6_BACFR	q64wy6 bacteroides
1172	73.5	6.2	563	2	Q64WY6_BACFR	q64wy6 bacteroides
1173	73.5	6.2	563	2	Q5LG29_BACFN	q5lg29 bacteroides
1174	73.5	6.2	570	1	Q7PFV1_ANOGA	q7pfv1 anopheles g
1175	73.5	6.2	574	2	Q8VZE2_ARATH	q8vze2 arabidopsis
1176	73.5	6.2	574	2	Q8VZE2_ARATH	q8vze2 arabidopsis
1177	73.5	6.2	607	2	Q5ATP6_EMENI	q5atp6 aspergillus
1178	73.5	6.2	614	2	Q3N230_9DELT	q3n230 syntrophoba
1179	73.5	6.2	634	2	O93990_CANAL	o93990 candida alb
1180	73.5	6.2	634	1	O93990_CANAL	o93990 candida alb
1181	73.5	6.2	634	2	Q6DFJ5_XENLA	q6dfj5 xenopus lae
1182	73.5	6.2	637	1	Q5CE41_CRYHO	q5ce41 cryptospori
1183	73.5	6.2	640	1	Q3R3X0_XYLFA	q3r3x0 xylella fas
1184	73.5	6.2	641	2	Q3R3X0_XYLFA	q3r3x0 xylella fas
1185	73.5	6.2	653	2	Q3REM6_XYLFA	q3rem6 xylella fas
1186	73.5	6.2	661	2	KUP_XYLFA	kup_xylfa xylella fas
1187	73.5	6.2	715	2	MUTL_BACHD	mutl_bachd bacillus ha
1188	73.5	6.2	731	1	APRN_ENTHI	aprn_enthi entamoeba h
1189	73.5	6.2	846	2	Q8TTHI_METAC	q8tthi methanosarc
1190	73.5	6.2	859	2	Q3NCP3_9PROT	q3ncp3 nitrosomona
1191	73.5	6.2	881	2	O68468_CORAM	o68468 corynebacte
1192	73.5	6.2	992	2	Q5IWR5_GLYGR	q5iwr5 glyceria gr
1193	73.5	6.2	1006	2	Q16531_CAEEL	q16531 caenorhabdi
1194	73.5	6.2	1019	2	Q93U53_CARRU	q93u53 carsonella
1195	73.5	6.2	1049	2	Q4YQY1_PLABE	q4yqy1 plasmodium
1196	73.5	6.2	1095	2	Q5ZM0_CHICK	q5zm0 gallus gall
1197	73.5	6.2	1100	2	Q5I31S_ENTHI	q5i31s entamoeba h
1198	73.5	6.2	1174	2	Q4YH96_PLABE	q4yh96 plasmodium
1199	73.5	6.2	1175	2	Q4HDG2_CAMCO	q4hdg2 campylobact

No.			Len	N	Accession	ID / Organism
1200	73.5	6.2	1277	2	Q76G00_CIOIN	q76g00 ciona intes
1201	73.5	6.2	1287	2	Q7YU59_DROME	q7yu59 drosophila
1202	73.5	6.2	1287	2	Q9U5W1_DROME	q9u5w1 drosophila
1203	73.5	6.2	1287	2	Q9VL24_DROME	q9vl24 drosophila
1204	73.5	6.2	1292	2	Q9AIH0_CARRU	q9aih0 carsonella
1205	73.5	6.2	1476	2	Q965D3_DICDI	q965d3 dictyosteli
1206	73.5	6.2	1545	2	Q8GU65_ORYSA	q8gu65 oryza sativ
1207	73.5	6.2	2666	2	Q6FW99_CANGA	q6fw99 candida gla
1208	73.5	6.2	3007	2	Q9DTE6_TETNG	q9dte6 tetraodon n
1209	73.5	6.2	3010	2	Q4SSR8_TETNG	q4ssr8 tetraodon n
1210	73.5	6.2	3381	2	Q9DTE6_9HEPC	q9dte6 hepatitis c
1211	73.5	6.2	4470	2	Q8IDK4_PLAF7	q8idk4 plasmodium
1212	73.5	6.2	4839	2	Q66WN5_9CORO	q66wn5 murine hepa
1213	73.5	6.2	7176	1	Q2N3S8_POLCB	q2n3s8 polyangium
1214	73.5	6.2	7178	1	RIAB_CVMA5	riab_cvma5 m replicase
1215	73	6.1	114	2	Q66WN6_9CORO	q66wn6 murine hepa
1216	73	6.1	114	2	Q75XA7_HELPY	q75xa7 helicobacte
1217	73	6.1	138	2	Q92LU2_HELPJ	q92lu2 helicobacte
1218	73	6.1	138	2	Q977T7_ELEMA	q977t7 elephas max
1219	73	6.1	140	2	Q37328_RHOPA	q37328 rhodopseudo
1220	73	6.1	145	2	Q64145_9MURI	q64145 ratus sp.
1221	73	6.1	155	1	Q9UXB0_SULSO	q9uxb0 sulfolobus
1222	73	6.1	155	2	Q7VJP1_HELHP	q7vjp1 helicobacte
1223	73	6.1	156	2	Q81510_9HEPC	q81510 hepatitis c
1224	73	6.1	156	2	Q81522_9HEPC	q81522 hepatitis c
1225	73	6.1	163	2	Q81537_9HEPC	q81537 hepatitis c
1226	73	6.1	220	2	Q80RY8_9HEPC	q80ry8 hepatitis c
1227	73	6.1	223	2	Q72240_BACC1	q72240 bacillus ce
1228	73	6.1	223	1	Q91S97_9CORO	q91s97 avian infec
1229	73	6.1	226	2	Q7T9P6_9CORO	q7t9p6 infectious
1230	73	6.1	238	1	Q81986_BACCR	q81986 infectious
1231	73	6.1	238	2	Q4MJ45_BACCE	q4mj45 bacillus ce
1232	73	6.1	238	2	Q636E3_BACCZ	q636e3 bacillus ce
1233	73	6.1	238	2	Q73216_BACC1	q73216 bacillus ce
1234	73	6.1	245	2	Q362R1_BACCI	q362r1 shewanella
1235	73	6.1	249	2	Q48TQ7_STRPM	q48tq7 streptococc
1236	73	6.1	249	2	Q48TG7_STRPM	q48tg7 streptococc
1237	73	6.1	249	1	Q7DAL8_STRP1	q7dal8 streptococc
1238	73	6.1	255	2	Q9FDU6_STRPY	q9fdu6 streptococc
1239	73	6.1	255	2	Q9YNU0_EAV	q9ynu0 equine arte
1240	73	6.1	264	2	Q9QN39_ANOGA	q9qn39 anopheles g
1241	73	6.1	264	1	P87639_EAV	p87639 equine arte
1242	73	6.1	264	2	Q8DAQ9_VIBVU	q8daq9 vibrio vuln
1243	73	6.1	264	2	Q36T98_MARHY	q36t98 marinobacte
1244	73	6.1	269	2	Q30RA4_THIDN	q30ra4 thiomicrosp
1245	73	6.1	273	2	Q2K662_RHIET	q2k662 rhizobium e
1246	73	6.1	279	1	Q6TY95_9BILA	q6ty95 xiphinema a
1247	73	6.1	282	1	NU2M_CAEEL	nu2m_caeel caenorhabdi
1248	73	6.1	290	1	Q5HGI3_STAAC	q5hgi3 staphylococ
1249	73	6.1	290	2	Q6G9W4_STAAS	q6g9w4 staphylococ
1250	73	6.1	290	2	Q8NX00_STAAW	q8nx00 staphylococ
1251	73	6.1	294	2	Q4X7M3_PLACH	q4x7m3 plasmodium
1252	73	6.1	294	2	Q4XT47_PLACH	q4xt47 plasmodium
1253	73	6.1	295	2	Q5AZG6_EMENI	q5azg6 aspergillus
1254	73	6.1	295	2	Q2XDN0_PSEPU	q2xdn0 pseudomonas
1255	73	6.1	295	2	Q8VUQ2_PSEPU	q8vuq2 pseudomonas
1256	73	6.1	295	2	Q88PN3_PSEPK	q88pn3 pseudomonas
1257	73	6.1	303	2	Q94EJ0_ARATH	q94ej0 arabidopsis
1258	73	6.1	314	2	Q2KDV3_RHIET	q2kdv3 rhizobium e
1259	73	6.1	315	2	Q2K5Y6_RHIET	q2k5y6 rhizobium e
1260	73	6.1	319	2	Q9H6T9_HUMAN	q9h6t9 homo sapien
1261	73	6.1	326	2	Q99NR7_MUSAV	q99nr7 muscardini
1262	73	6.1	326	2	Q99NR7_MUSAV	q99nr7 muscardini
1263	73	6.1	335	2	Q8SWL8_ENCCU	q8swl8 encephalito
1264	73	6.1	335	1	SRG7_CAEEL	srg7_caeel caenorhabdi
1265	73	6.1	340	2	Q9N2T2_CAEEL	q9n2t2 caenorhabdi
1266	73	6.1	343	2	Q7YFU0_9HYME	q7yfu0 cynolebias
1267	73	6.1	348	2	Q85AS7_UMASC	q85as7 uma scopari
1268	73	6.1	358	1	Q4E9M7_9RICK	q4e9m7 myrmica sul
1269	73	6.1	364	2	Q99P50_9MEG	q99p50 wolbachia e
1270	73	6.1	364	1	GHSR_MOUSE	ghsr_mouse mus musculu
1271	73	6.1	364	1	GHSR_RAT	ghsr_rat ratus norv
1272	73	6.1	375	2	Q86NC0_CAEEL	q86nc0 caenorhabdi

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1273	73	6.1	378	2	Q70EG4_9RODE	saccostomus	Q70eg4 saccostomus
1274	73	6.1	378	2	Q70EG5_9RODE	saccostomus	Q70eg5 saccostomus
1275	73	6.1	379	1	CYB_CRAFU	cratogeomys	Q8wdv6 cratogeomys
1276	73	6.1	379	2	Q34099_CRAFU	cratogeomys	Q34099 cratogeomys
1277	73	6.1	379	2	Q698Q2_CRAFU	cratogeomys	Q698q2 cratogeomys
1278	73	6.1	379	2	Q8WDV7_CRATY	cratogeomys	Q8wdv7 cratogeomys
1279	73	6.1	383	2	Q9GL20_CYNSP	cynopterus	Q9gl20 cynopterus
1280	73	6.1	391	2	Y450_BUCAP	buchnera ap	Y450_bucap buchnera ap
1281	73	6.1	394	2	Q6EE99_LATCH	latimeria c	Q6ee99 latimeria c
1282	73	6.1	396	2	Q3F4A7_9BURK	burkholderi	Q3f4a7 burkholderi
1283	73	6.1	396	2	Q44YS3_9BURK	burkholderi	Q44ys3 burkholderi
1284	73	6.1	396	2	Q39KD3_BURS3	burkholderi	Q39kd3 burkholderi
1285	73	6.1	399	2	Q6L0J3_PICTO	picrophilus	Q6l0j3 picrophilus
1286	73	6.1	401	2	Q6KZX3_PICTO	picrophilus	Q6kzx3 picrophilus
1287	73	6.1	412	2	Q61M38_CAEBR	rhodopseudo	Q61m38 rhodopseudo
1288	73	6.1	414	2	Q34D58_RHOPA	caenorhabdi	Q34d58 caenorhabdi
1289	73	6.1	424	2	Q3ISS0_NATPD	natronomona	Q3iss0 natronomona
1290	73	6.1	437	2	Q3AVM8_SYNS9	synechococc	Q3avm8 synechococc
1291	73	6.1	446	2	Q4YN50_PLABE	plasmodium	Q4yn50 plasmodium
1292	73	6.1	450	2	Q8H9B3_BRACM	brassica ca	Q8h9b3 brassica ca
1293	73	6.1	450	1	VGLM_EHV1B	equine herp	Q6s6v2 equine herp
1294	73	6.1	450	2	Q6S6V2_9ALPH	equid herpe	Q6s6v2 equid herpe
1295	73	6.1	452	2	Q36010_9GAMM	shewanella	Q36010 shewanella
1296	73	6.1	453	2	Q94307_CAEBL	caenorhabdi	Q94307 caenorhabdi
1297	73	6.1	461	2	Q4K0J6_STRPN	streptococc	Q4k0j6 streptococc
1298	73	6.1	461	2	Q9R923_STRPN	streptococc	Q9r923 streptococc
1299	73	6.1	470	2	Q54PF0_DICDI	dictyosteli	Q54pf0 dictyosteli
1300	73	6.1	474	2	Q94CI7_ARATH	arabidopsis	Q94ci7 arabidopsis
1301	73	6.1	481	2	Q4K4Z1_PSEF5	pseudomonas	Q4k4z1 pseudomonas
1302	73	6.1	487	2	Q37NN7_RHOPA	rhodopseudo	Q37nn7 rhodopseudo
1303	73	6.1	487	2	Q7MBA5_PHOLL	photorhabdu	Q7mba5 photorhabdu
1304	73	6.1	488	2	Q4HRT1_CAMUP	campylobact	Q4hrt1 campylobact
1305	73	6.1	494	1	KCNF1_HUMAN	homo sapien	Q58sl3 homo sapien
1306	73	6.1	494	2	Q58SL3_HUMAN	homo sapien	Q58sl3 homo sapien
1307	73	6.1	509	2	Q5CUK7_CRYPV	cryptospori	Q5cuk7 cryptospori
1308	73	6.1	510	2	Q27072_TAESO	taenia soli	Q27072 taenia soli
1309	73	6.1	520	2	Q5KWR7_GEOKA	geobacillus	Q5kwr7 geobacillus
1310	73	6.1	525	2	Q44MH7_CHLLI	chlorobium	Q44mh7 chlorobium
1311	73	6.1	546	2	Q5EAY8_XENLA	xenopus lae	Q5eay8 xenopus lae
1312	73	6.1	553	2	Q3MP12_CANAL	candida alb	Q3mp12 candida alb
1313	73	6.1	553	2	Q59PN9_CANAL	candida alb	Q59pn9 candida alb
1314	73	6.1	553	2	Q9ZJ35_HELPJ	helicobacte	Q9zj35 helicobacte
1315	73	6.1	556	2	Q7QZJ9_GIALA	giardia lam	Q7qzj9 giardia lam
1316	73	6.1	597	2	Q2SRQ8_MYCCA	mycoplasma	Q2srq8 mycoplasma
1317	73	6.1	599	2	Q3Y0F7_ENTFC	enterococcu	Q3y0f7 enterococcu
1318	73	6.1	599	2	Q3V5J8_CAEBL	caenorhabdi	Q3v5j8 caenorhabdi
1319	73	6.1	604	2	Q6B1Q1_DEBHA	debaryomyce	Q6b1q1 debaryomyce
1320	73	6.1	616	2	Q4RMH4_TETNG	tetraodon n	Q4rmh4 tetraodon n
1321	73	6.1	623	2	Q86X77_HUMAN	homo sapien	Q86x77 homo sapien
1322	73	6.1	635	2	Q7NBK6_MYCGA	mycoplasma	Q7nbk6 mycoplasma
1323	73	6.1	643	2	Q9ALX8_BURPS	burkholderi	Q9alx8 burkholderi
1324	73	6.1	668	2	Q63L6L_BURPS	burkholderi	Q63l6l burkholderi
1325	73	6.1	668	2	Q9VF31_DROME	drosophila	Q9vf31 drosophila
1326	73	6.1	676	2	Q2WL35_CLOBE	clostridium	Q2wl35 clostridium
1327	73	6.1	676	2	Q4W5R5_CAEBL	caenorhabdi	Q4w5r5 caenorhabdi
1328	73	6.1	703	2	Q59LX3_CANAL	candida alb	Q59lx3 candida alb
1329	73	6.1	716	2	Q59LX3_CANAL	caenorhabdi	Q59lx3 caenorhabdi
1330	73	6.1	788	1	FTSK_STAAN	staphylococ	P64165 staphylococ
1331	73	6.1	788	1	FTSK_STAAC	staphylococ	P64164 staphylococ
1332	73	6.1	788	1	FTSK_STAAM	staphylococ	Q5hgf5 staphylococ
1333	73	6.1	789	1	FTSK_STAAR	oryza sativ	Q5z6j8 oryza sativ
1334	73	6.1	806	2	Q5Z6J8_ORYSA	rhodopirell	Q7uqf9 rhodopirell
1335	73	6.1	832	2	Q7UQF9_RHOBA	picrophilus	Q6kyt8 picrophilus
1336	73	6.1	844	2	Q6KYT8_PICTO	trypanosoma	Q4dil4 trypanosoma
1337	73	6.1	861	2	Q4DIL4_TRYCR	guillardia	Q9avx8 guillardia
1338	73	6.1	861	2	Q9AVX8_GUITH	mus musculu	Q9avx8 mus musculu
1339	73	6.1	966	2	PKD2_MOUSE	mus musculu	Q7tsi7 mus musculu
1340	73	6.1	966	2	Q7TSI7_MOUSE	mus musculu	Q35245 mus musculu
1341	73	6.1	971	2	Q35245_MOUSE	homo sapien	O60337 homo sapien
1342	73	6.1	1035	2	O60337_HUMAN	schistosoma	Q967w1 schistosoma
1343	73	6.1	1052	2	Q8BPR6_MOUSE	exiguobacte	O60337 exiguobacte
1344	73	6.1	1075	2	Q967W1_SCHMA	arabidopsis	Q9lpe2 arabidopsis
1345	73	6.1	1111	2	Q86FP2_CAEBL	caenorhabdi	Q86fp2 caenorhabdi
1346	73	6.1	1127	2	Q9N323_CAEBL	caenorhabdi	Q9n323 caenorhabdi
1347	73	6.1	1156	2	Q4WGM4_ASPFU	aspergillus	Q4wgm4 aspergillus
1348	73	6.1	1268	2	Q55JT5_DICDI	dictyosteli	Q55jt5 dictyosteli
1349	73	6.1	1931	2	Q8RJY3_STIAU	stigmatella	Q8rjy3 stigmatella
1350	73	6.1	1951	2	Q7PZN7_ANOGA	anopheles g	Q7pzn7 anopheles
1351	73	6.1	3010	2	P88803_9HEPC	hepatitis c	P88803 hepatitis c
1352	73	6.1	3010	2	Q9J3G1_9HEPC	hepatitis c	Q9j3g1 hepatitis c
1353	73	6.1	3010	2	Q9J3I0_9HEPC	hepatitis c	Q9j3i0 hepatitis c
1354	73	6.1	3013	2	Q9QIX9_9HEPC	hepatitis c	Q9qix9 hepatitis c
1355	73	6.1	3013	2	Q9QIY0_9HEPC	hepatitis c	Q9qiy0 hepatitis c
1356	73	6.1	6875	2	Q28733_CANAL	candida alb	Q28733 candida alb
1357	72.5	6.1	105	2	Q5ALK7_CANAL	candida alb	Q5alk7 candida alb
1358	72.5	6.1	144	2	Q2LWL0_9DELT	syntrophus	Q2lwl0 syntrophus
1359	72.5	6.1	156	2	Q81516_9HEPC	hepatitis c	Q81516 hepatitis c
1360	72.5	6.1	156	2	Q81519_9HEPC	hepatitis c	Q81519 hepatitis c
1361	72.5	6.1	167	2	Q5KIU4_CRYNE	cryptococcu	Q5kiu4 cryptococcu
1362	72.5	6.1	170	2	Q2ULP6_ASPOR	aspergillus	Q2ulp6 aspergillus
1363	72.5	6.1	173	2	Q9WD17_EAV	equine arte	Q9wd17 equine arte
1364	72.5	6.1	174	2	P97065_9ENTR	salmonella	P97065 salmonella
1365	72.5	6.1	180	2	P71252_ECOLI	escherichia	P71252 escherichia
1366	72.5	6.1	180	2	P71253_ECOLI	escherichia	P71253 escherichia
1367	72.5	6.1	180	2	P71254_ECOLI	escherichia	P71254 escherichia
1368	72.5	6.1	180	2	P71255_ECOLI	escherichia	P71255 escherichia
1369	72.5	6.1	180	2	P71256_ECOLI	escherichia	P71256 escherichia
1370	72.5	6.1	180	2	P71258_ECOLI	escherichia	P71258 escherichia
1371	72.5	6.1	180	2	P71259_ECOLI	escherichia	P71259 escherichia
1372	72.5	6.1	180	2	P71260_ECOLI	escherichia	P71260 escherichia
1373	72.5	6.1	183	2	P71261_ECOLI	escherichia	P71261 escherichia
1374	72.5	6.1	191	2	Q55TU2_CRYNE	cryptococcu	Q55tu2 cryptococcu
1375	72.5	6.1	208	2	Q8U4P0_PYRFU	pyrococcus	Q8u4p0 pyrococcus
1376	72.5	6.1	208	2	Q63447_ECHDI	echinotrix	Q63447 echinotrix
1377	72.5	6.1	209	2	Q8GZ10_ARATH	arabidopsis	Q8gz10 arabidopsis
1378	72.5	6.1	209	2	Q49834_MYCLE	mycobacteri	Q49834 mycobacteri
1379	72.5	6.1	210	2	Q7JY19_ECHDI	echinotrix	Q7jy19 echinotrix
1380	72.5	6.1	210	2	Q7JTL3_ECHDI	echinotrix	Q7jtl3 echinotrix
1381	72.5	6.1	211	2	Q7JT13_ECHDI	echinotrix	Q7jt13 echinotrix
1382	72.5	6.1	214	2	Q63950_ECHDI	echinotrix	Q63950 echinotrix
1383	72.5	6.1	217	2	Q9XMK7_OCHPR	ochotona pr	Q9xmk7 ochotona pr
1384	72.5	6.1	220	2	Q40J90_EHRCH	ehrlichia c	Q40j90 ehrlichia
1385	72.5	6.1	222	2	Q31Y29_SHIBS	shigella bo	Q31y29 shigella bo
1386	72.5	6.1	222	2	Q3YZU8_SHIBS	shigella so	Q3yzu8 shigella so
1387	72.5	6.1	224	2	Q8RGE6_FUSNN	fusobacteri	Q8rge6 fusobacteri
1388	72.5	6.1	243	2	Q4MHS9_BACCE	bacillus ce	Q4mhs9 bacillus ce
1389	72.5	6.1	255	2	Q7M2C0_LEIAM	leishmania	Q7m2c0 leishmania
1390	72.5	6.1	267	2	Q3HA88_TRIER	trichodesmi	Q3ha88 trichodesmi
1391	72.5	6.1	267	2	Q4S673_TETNG	tetraodon n	Q4s673 tetraodon n
1392	72.5	6.1	285	2	Q8RSS9_FUSNN	fusobacteri	Q8rss9 fusobacteri
1393	72.5	6.1	285	2	Q86DD6_CAEBL	caenorhabdi	Q86dd6 caenorhabdi
1394	72.5	6.1	288	2	Q2WLM6_CLOBE	clostridium	Q2wlm6 clostridium
1395	72.5	6.1	291	1	O24561_MAIZE	zea mays (m	O24561 zea mays
1396	72.5	6.1	298	2	Q5WL74_BACSK	bacillus cl	Q5wl74 bacillus cl
1397	72.5	6.1	298	2	Q8R2A8_MOUSE	mus musculu	Q8r2a8 mus musculu
1398	72.5	6.1	307	2	Q612V8_CAEBR	caenorhabdi	Q612v8 caenorhabdi
1399	72.5	6.1	308	2	Q6N472_RHOPA	rhodopseudo	Q6n472 rhodopseudo
1400	72.5	6.1	309	2	Q71UE1_BOVIN	bos taurus	Q71ue1 bos taurus
1401	72.5	6.1	310	2	Q71UD1_BOVIN	chimarrogal	Q5j2f7 chimarrogal
1402	72.5	6.1	310	2	Q5J2F7_CHIHI	bacillus cl	Q5wp84 bacillus cl
1403	72.5	6.1	315	2	Q5WP84_9DIPT	dermatobia	Q5wb84 dermatobia
1404	72.5	6.1	315	2	Q5WB84_9DIPT	staphylococ	Q9lgo2 staphylococ
1405	72.5	6.1	320	1	Q9LGO2_ARATH	oryza sativ	Q91g02 oryza sativ
1406	72.5	6.1	325	2	Q91G02_ARATH	lactococcus	Q9ch29 lactococcus
1407	72.5	6.1	326	2	Q9CH29_LACLA	lactococcus	Q9ci19 lactococcus
1408	72.5	6.1	348	2	Q9CI19_LACLA	caenorhabdi	O17077 caenorhabdi
1409	72.5	6.1	348	2	O17077_CAEBL	enterococcu	Q833b9 enterococcu
1410	72.5	6.1	350	2	Q833B9_ENTFA	cyprinella	Q99924 cyprinella
1411	72.5	6.1	355	2	Q99924_9TELE	enterococcu	O83512 enterococcu
1412	72.5	6.1	356	2	O83512_ENTFA	escherichia	Q5ues6 escherichia
1413	72.5	6.1	356	2	Q5UES6_ECOLI	escherichia	Q57a42 escherichia
1414	72.5	6.1	356	2	Q57A42_BRUAB	brucella ab	Q2yif9 brucella ab
1415	72.5	6.1	360	2	Q2YIF9_BRUAB	brucella ab	Q8fxm4 brucella ab
1416	72.5	6.1	363	2	Q8FXM4_BRUSU	brucella su	O70us3 brucella su
1417	72.5	6.1	365	2	Q41629_STAHJ	bacillus th	Q41629 staphylococ
1418	72.5	6.1	374	2	Q8WMR0_SHEEP	ovis aries	Q8wmr0 ovis aries

No.			Len		ID	Accession	Organism
1419	72.5	6.1	377	2	Q4R215_VARHI	Q4r215	vargula hil
1420	72.5	6.1	379	1	CYB_CHHI	Q85av3	chimarrogal
1421	72.5	6.1	379	1	CYB_OCHAL	Q9gby1	ochotona al
1422	72.5	6.1	379	1	CYB_OCHCU	Q9g1b9	ochotona cu
1423	72.5	6.1	379	1	CYB_OCHHI	Q9gby6	ochotona hi
1424	72.5	6.1	379	1	CYB_OCHHY	Q9g6g2	ochotona hy
1425	72.5	6.1	379	1	CYB_OCHHY	Q9gbz0	ochotona hy
1426	72.5	6.1	379	1	CYB_OCHKO	Q9gbz1	ochotona ko
1427	72.5	6.1	379	1	CYB_OCHLA	Q9gbz1	ochotona la
1428	72.5	6.1	379	1	CYB_OCHNB	Q9gbz2	ochotona nu
1429	72.5	6.1	379	1	CYB_OCHRO	Q9gbz2	ochotona ro
1430	72.5	6.1	379	1	CYB_OCHRU	Q9gbz5	ochotona ru
1431	72.5	6.1	379	1	CYB_OCHTH	Q9gbz6	ochotona th
1432	72.5	6.1	379	1	CYB_OCHTI	Q9gbz7	ochotona ti
1433	72.5	6.1	379	1	Q3LHY6_CHIPT	Q3lhy6	chimarrogal
1434	72.5	6.1	379	1	Q3LHY7_CHIPT	Q3lhy7	chimarrogal
1435	72.5	6.1	379	2	Q3LHZ0_CHIPT	Q3lhz0	chimarrogal
1436	72.5	6.1	379	2	Q3LHZ2_CHIPT	Q3lhz2	chimarrogal
1437	72.5	6.1	379	2	Q3LHZ7_CHIPT	Q3lhz7	chimarrogal
1438	72.5	6.1	379	2	Q3LI03_CHIPT	Q3li03	chimarrogal
1439	72.5	6.1	379	2	Q3LI07_CHIPT	Q3li07	chimarrogal
1440	72.5	6.1	379	2	Q3LI15_CHIPT	Q3li15	chimarrogal
1441	72.5	6.1	379	2	Q3LI18_CHIPT	Q3li18	chimarrogal
1442	72.5	6.1	379	2	Q3LI31_CHIPT	Q3li31	chimarrogal
1443	72.5	6.1	379	2	Q3LI32_CHIPT	Q3li32	chimarrogal
1444	72.5	6.1	379	2	Q3LI39_CHIPT	Q3li39	chimarrogal
1445	72.5	6.1	379	2	Q3LI49_CHIPT	Q3li49	chimarrogal
1446	72.5	6.1	379	2	Q71LX8_9LAGO	Q71lx8	ochotona ca
1447	72.5	6.1	379	2	Q9G1C3_9LAGO	Q9g1c3	ochotona ca
1448	72.5	6.1	379	2	Q9G1C4_9LAGO	Q9g1c4	ochotona an
1449	72.5	6.1	379	2	Q9GBY2_9LAGO	Q9gby2	ochotona ca
1450	72.5	6.1	379	2	Q9GBY8_9LAGO	Q9gby8	ochotona hu
1451	72.5	6.1	379	2	Q9GBY9_OCHHY	Q9gby9	ochotona hy
1452	72.5	6.1	379	2	Q9GBZ3_OCHPA	Q9gbz3	ochotona pa
1453	72.5	6.1	389	2	Q8EWI6_MYCPE	Q8ewi6	mycoplasma
1454	72.5	6.1	379	2	Q50BJ4_9RODE	Q50bj4	perognathus
1455	72.5	6.1	379	2	Q50BJ6_PERPA	Q50bj6	perognathus
1456	72.5	6.1	379	2	Q50BP1_MICMC	Q50bp1	microdipodo
1457	72.5	6.1	379	2	Q50BP2_9RODE	Q50bp2	microdipodo
1458	72.5	6.1	379	2	Q9GAW7_9RODE	Q9gaw7	chaetodipus
1459	72.5	6.1	387	2	Q6RKP6_EBVG	Q6rkp6	epstein-bar
1460	72.5	6.1	388	2	Q2MDP6_CROCR	Q2mdp6	crocuta cro
1461	72.5	6.1	389	2	Q2MDP6_CROCR	Q2mdp6	crocuta cro
1462	72.5	6.1	395	2	OXYR_HUMAN	P30559	homo sapien
1463	72.5	6.1	395	2	O32827_SHIDS	O32827	shigella dy
1464	72.5	6.1	402	2	O8WMQ9_SHEEP	O8wmq9	ovis aries
1465	72.5	6.1	404	2	O2SCC2_9GAMM	O2scc2	hahella che
1466	72.5	6.1	428	2	Q66CF9_YERPS	Q66cf9	yersinia ps
1467	72.5	6.1	428	2	O82G86_YERPE	O82g86	yersinia pe
1468	72.5	6.1	435	2	O31E26_THICR	O31e26	thiomicrosp
1469	72.5	6.1	442	2	O61OY3_PICTO	O61oy3	picrophilus
1470	72.5	6.1	442	2	O6PHK5_BRARE	O6phk5	brachydanio
1471	72.5	6.1	445	2	O6NYH8_BRARE	O6nyh8	brachydanio
1472	72.5	6.1	452	2	Q9T9N6_9BILA	Q9t9n6	terebratuli
1473	72.5	6.1	457	2	O6P822_XENTR	O6p822	xenopus tro
1474	72.5	6.1	478	2	O97OD2_SULTO	O97od2	sulfolobus
1475	72.5	6.1	488	2	Q4HEC1_CAMCO	Q4hec1	campylobact
1476	72.5	6.1	488	2	Q4HLMO_CAMLA	Q4hlmo	campylobact
1477	72.5	6.1	491	2	O6SWL8_HCMV	O6swl8	human cytom
1478	72.5	6.1	499	1	MVIN_AQUAE	O67658	aquifex aeo
1479	72.5	6.1	505	2	O8QRY6_9BETA	O8qry6	pongine her
1480	72.5	6.1	509	1	PACR_BOVIN	O8aPj8	bos taurus
1481	72.5	6.1	513	1	O4API8_9CHLB	O4api8	chlorobium
1482	72.5	6.1	521	1	Q2RIT1_MOOTH	Q2rit1	moorella th
1483	72.5	6.1	521	2	Q4QLL3_HAEI8	Q4qll3	haemophilus
1484	72.5	6.1	522	2	Q23444_CAEEL	Q23444	caenorhabdi
1485	72.5	6.1	526	2	Q6FDF6_ACIAD	Q6fdf6	acinetobact
1486	72.5	6.1	528	2	Q40LE0_DESAC	Q40le0	desulfuromo
1487	72.5	6.1	528	2	Q4RQ12_TETNG	Q4rq12	tetraodon n
1488	72.5	6.1	539	2	Q5CU37_CRYPV	Q5cu37	cryptospori
1489	72.5	6.1	539	2	Q7VSL1_BORPE	Q7vsl1	bordetella
1490	72.5	6.1	539	2	Q7W446_BORPA	Q7w446	bordetella
1491	72.5	6.1	562	2	Q7WFK3_BORPA	Q7wfk3	bordetella
	72.5	6.1			Q5FIM1_MYTGA	Q5fim1	mytilus gal
1492	72.5	6.1	567	2	Q4YTZ9_PLABE	Q4ytz9	plasmodium
1493	72.5	6.1	574	2	Q2X1N5_9GAMM	Q2x1n5	shewanella
1494	72.5	6.1	574	2	Q2X1N5_9GAMM	Q2x1n5	shewanella
1495	72.5	6.1	574	2	Q35VD8_9GAMM	Q35vd8	shewanella
1496	72.5	6.1	580	2	Q6LH28_PHOPR	Q6lh28	photobacter
1497	72.5	6.1	614	2	Q3X6Y0_METFL	Q3x6y0	methylobaci
1498	72.5	6.1	614	2	Q34X67_9GAMM	Q34x67	alkalilimni
1499	72.5	6.1	622	2	Q7U5J3_SYNPX	Q7u5j3	synechococc
1500	72.5	6.1	635	2	Q4B546_9BURK	Q4b546	polaromonas
					O21335_CAEEL	O21335	caenorhabdi

ALIGNMENTS

RESULT 1

MENTO_HUMAN

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ID   MENTO_HUMAN    STANDARD;    PRT;   234 AA.
AC   O95772;
DT   15-NOV-2002, integrated into UniProtKB/Swiss-Prot.
DT   01-MAY-1999, sequence version 1.
DT   07-FEB-2006, entry version 39.
DE   MLN64 N-terminal domain homolog (STARD3 N-terminal-like protein).
GN   Name=STARD3NL; Synonyms=MENTHO; ORFNames=UNQ855/PRO1864;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE, CHARACTERIZATION, TOPOLOGY, PHOSPHORYLATION, AND
RP   ALTERNATIVE INITIATION.
RC   TISSUE=Fetal brain;
RX   MEDLINE=22384343; PubMed=12393907; DOI=10.1074/jbc.M208290200;
RA   Alpy F., Wendling C., Rio M.-C., Tomasetto C.;
RT   "MENTHO, a MLN64 homologue devoid of the START domain.";
RL   J. Biol. Chem. 277:50780-50787(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA   Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA   Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA   Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA   Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA   Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA   Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA   Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA   Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA   Kozlowicz-Reilly A., Leonard S., Rohling T., Rock S.M.,
RA   Tin-Wollam A.-M., Abbott J., Minx P., Maupin R., Strowmatt C.,
RA   Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
RA   Wendl M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,
RA   Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
RA   Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA   Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
RA   Gillett W., Zhou Y., James R., Phelps K., Iadanoto S., Bubb K.,
RA   Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
RA   Baertsch R.A., Brent M.R., Keibler E., Flicek P., Bork P., Suyama M.,
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RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7.";
RL Nature 424:157-164(2003).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX TISSUE=Brain, and Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
    membrane protein.
-!- ALTERNATIVE PRODUCTS:
    Event=Alternative initiation; Named isoforms=2;
    Comment=Alternative initiation;
    Name=1 (shown here) and 2, are produced by
    alternative initiation;
-!- PTM: Phosphorylated.
-!- SIMILARITY: Contains 1 MENTAL domain.

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----
DR EMBL; AJ492267; CAD37353.1; -; mRNA.
DR EMBL; AY358645; AAQ89008.1; -; mRNA.
DR EMBL; AC006033; -; -; Genomic_DNA.
DR EMBL; BC003074; AAH03074.1; -; mRNA.
DR EMBL; BC005959; AAH05959.1; -; mRNA.
DR HGNC; HGNC:19169; STARD3NL.
DR Ensembl; ENSG00000010270; Homo sapiens.
KW Alternative initiation; Membrane; Phosphorylation; Transmembrane.
FT CHAIN   1   234   MLN64 N-terminal domain homolog, isoform
FT   1.
FT   /FTId=PRO_000021666.
FT CHAIN   8   234   MLN64 N-terminal domain homolog, isoform
FT   2.
FT   /FTId=PRO_000021667.
FT INIT_MET   8   8   For isoform 2.
FT TOPO_DOM   1   53   Cytoplasmic (Potential).
FT TRANSMEM   54   74   Potential.
FT TOPO_DOM   75   97   Extracellular (Potential).
FT TRANSMEM   98   118   Potential.
FT TOPO_DOM 119   122   Cytoplasmic (Potential).
FT TRANSMEM 123   143   Potential.
FT TOPO_DOM 144   150   Extracellular (Potential).
FT TRANSMEM 151   171   Potential.
FT TOPO_DOM 172   218   Cytoplasmic (Potential).
FT DOMAIN   48   218   MENTAL.
SQ SEQUENCE 234 AA; 26655 MW; AFB7DAE381983FB0 CRC64;

Query Match   100.0%; Score 1195; DB 1; Length 234;
Best Local Similarity   100.0%;
Matches 234; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy 1 MNHLPEDMENALTGSQOSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT 60

Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MNHLPEDMENALTGSQOSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT 60

Qy 61 FDLLFVTLLMWIIELNVNGGIENTLEKEVMQYDYSSSYFDIFLLLAVFRFKVLILAYAVCRL 120

Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 FDLLFVTLLMWIIELNVNGGIENTLEKEVMQYDYSSSYFDIFLLLAVFRFKVLILAYAVCRL 120

Qy 121 RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA 180

Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA 180

Qy 181 EEENRLLIVQDDASERAALIPGGLSDQGFYSPPESEAGSEEAEEKQDSEKPLLEL 234

Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 EEENRLLIVQDDASERAALIPGGLSDQGFYSPPESEAGSEEAEEKQDSEKPLLEL 234

RESULT 2
Q5U205_RAT
ID   Q5U205_RAT   PRELIMINARY;   PRT;   235 AA.
AC   Q5U205;
DT   07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT   07-DEC-2004, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   STARD3 N-terminal like (Predicted).
GN   Name=Stard3nl;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Ovary;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Ovary;
RG   NIH MGC Project;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.

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DR   EMBL; BC086352; AAH86352.1; -; mRNA.
DR   Ensembl; ENSRNOG00000012126; Rattus norvegicus.
SQ   SEQUENCE 235 AA; 26719 MW; 6238B671397EA775 CRC64;

Query Match   95.5%; Score 1141.5; DB 2; Length 235;
Best Local Similarity   95.7%;
Matches 225; Conservative   3; Mismatches   6; Indels   1; Gaps   1;

Qy 1 MNHLPEDMENALTGSQOSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT 60

```
Qy    1  MNHLPEDMENTLTGSQSSHASLRDIHSINPGQLMARIESYEGREKKGISDVRRTFCLFVT   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MNHLPEDMENTLTGSQSSHASLRDIHSINPGQLMARIESYEGREKKGISDVRRTFCLFVT   60

Qy   61  FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYPDIFLLAVRFKVLLLAYAVCRL    120
         |||||||||||||||| | ||| |||| || ||||||||||||||| |||||  ||||
Db   61  FDLLFVTLLWIIELNVNGGIENTLKVEVAHYDYSSYPDIFLLAVRFRKVLLLGYAVCRL   120

Qy  121  RHWWAIALTTAVTSAFLLAKVILSKLFSQGARGYVLPIISFILAWIETWFLDFKVLPQEA  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  RHWWAIALTTAVTSAFLLAKVILSKLFSQGARGYVLPIISFILAWIETWFLDFKVLPQEA  180

Qy  181  EEENRLLIVQDASERAALIPGGLSDGQFYSPPESEAGS-EEAEEKQDSEKPLLEL      234
         |||||||||||||||||||| |||||||||||||||| |||||||||||||||||
Db  181  EEENRLLIVQDASERAALIPAGLSDGQFYSPPESEAGSSEEEAEEKQDSEKPLLEL      235
```

RESULT 3
MENTO_MOUSE

ID   MENTO_MOUSE   STANDARD;   PRT;   235 AA.
AC   Q9DCI3; Q99J63; Q9D3S6;
DT   15-NOV-2002, integrated into UniProtKB/Swiss-Prot.
DT   15-NOV-2002, sequence version 2.
DT   07-FEB-2006, entry version 29.
DE   MLN64 N-terminal domain homolog (STARD3 N-terminal-like protein).
GN   Name=Stard3nl; Synonyms=Mentho;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum, and Kidney;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reid J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tonaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RL   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).

RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC   TISSUE=Mammary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RL   "Generation and initial analysis of more than 15,000 full-length human
RL   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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-!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
    membrane protein (By similarity).
-!- ALTERNATIVE PRODUCTS:
    Event=Alternative splicing; Named isoforms=2;
    Name=1;
      IsoId=Q9DCI3-1; Sequence=Displayed;
    Name=2;
      IsoId=Q9DCI3-2; Sequence=VSP_003909;
      Note=No experimental confirmation available;
-!- SIMILARITY: Contains 1 MENTAL domain.
-!- CAUTION: Ref.1 (BAB31166) sequence differs from that shown due to
    a frameshift in position 31.

DR   EMBL; AK002760; BAB22337.1; -; mRNA.
DR   EMBL; AK018331; BAB31166.1; ALT_FRAME; mRNA.
DR   EMBL; BC003334; AAH03334.1; -; mRNA.
DR   Ensembl; ENSMUSG00000003062; Mus musculus.
DR   MGI; MGI:1923455; Stard3nl.
KW   Alternative splicing; Membrane; Transmembrane.
FT   CHAIN   1   235   MLN64 N-terminal domain homolog.
FT   /FTId=PRO_000096420.
FT   TOPO_DOM   1   53   Cytoplasmic (Potential).
FT   TRANSMEM   54   74   Potential.
FT   TOPO_DOM   75   97   Extracellular (Potential).
FT   TRANSMEM   98   118   Potential.
FT   TOPO_DOM   119   122   Cytoplasmic (Potential).
FT   TRANSMEM   123   143   Potential.
FT   TOPO_DOM   144   150   Extracellular (Potential).
FT   TRANSMEM   151   171   Potential.
FT   TOPO_DOM   172   235   Cytoplasmic (Potential).
FT   DOMAIN   48   218   MENTAL.
FT   VARSPLIC   218   235   SEEEAEEKQDSEKPLLEL -> RNSSAFRMGIQKSSQPSGG
FT   AAGTRARFVPKASSCREGRPGLPWMLQ (in isoform
FT   2).
FT   /FTId=VSP_003909.
FT   CONFLICT   32   33   QL -> HS (in Ref. 1; BAB22337).
FT   CONFLICT   52   52   R -> G (in Ref. 2).
SQ   SEQUENCE   235 AA;   26811 MW;   F25172S390CB1503 CRC64;

Query Match   94.9%;   Score 1134.5; DB 1; Length 235;
Best Local Similarity   94.9%;   Pred. No. 1.2e-94;
Matches 223; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

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Qy   1  MNHLPEDMENALTTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT  60
        ||||||||||:|||||||||||||:|||||||:||||||||||||||||||||||||||||
Db   1  MNHLPEDMENTLTGSQSSHASLRDIHSINPAQLMARIESYEGREKKGISDVRRTFCLFVT   60
```

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Qy       61 FDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRL 120
            ||||||||||||:|::||||||||:|:||||||||||||||||||||||||||||||||
Db       61 FDLLFVTLLWIIELNVNGGIENTLKKEVIHYDYYSSYFDIFLLAVRFKVLILGYAVCRL 120

Qy      121 RHWWAIAITTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFFILAWIETWFLDFKVLPQEA 180
            ||||||||||||||:||||||||:||||||||||||||||||||||||||||||||||||
Db      121 RHWWAIAITTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFFILAWIETWFLDFKVLPQEA 180

Qy      181 EEENRLLIVQDASERAALIPGGLSDGQFYSPPESEAGS--EEAEEKQODSEKPLLEL 234
            |||||||||||||||||||||||||||||||||||||  |||||||||||||||||
Db      181 EEENRLLIVQDASERAALIPAGLSDGQFYSPPESEAGSEEEAEEKQESEKPLLEL 235
```

RESULT 4

ID   Q3U8Q7_MOUSE   PRELIMINARY;   PRT;   235 AA.
AC   Q3U8Q7;
Db   Q3U8Q7;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Bone marrow macrophage cDNA, RIKEN full-length enriched library,
DE   clone:I830047P07 product:STARD3 N-terminal like, full insert sequence.
GN   Name=Stard3nl;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
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RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
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RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
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RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [2]
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RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
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RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
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RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
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RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
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RN   [4]
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RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).

RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length-enriched cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
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RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Oyama R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
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RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura N., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

CC   -----------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; AK152116; BAE30960.1; -; mRNA.
DR   MGI; MGI:1923455; Stard3nl.
SQ   SEQUENCE   235 AA;   26811 MW;   F25172539DCB1503 CRC64;

Query Match   94.9%;   Score 1134.5;   DB 2;   Length 235;
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DT   11-OCT-2005, sequence version 1.
DT   07-FEB-2006, entry version 5.
DE   Bone marrow macrophage cDNA, RIKEN full-length enriched library,
DE   clone:I830067H03 product:STARD3 N-terminal like, full insert sequence.
GN   Name=Stard3nl;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.

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RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
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RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
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RL Nature 409:685-690(2001).
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RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
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RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima H., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,

RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC ---
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC ---
DR EMBL; AK152378; BAE31167.1; -; mRNA.
DR MGI; MGI:1923455; Stard3nl.
SQ SEQUENCE 235 AA; 26777 MW; AD551A8C9FCF73D8 CRC64;

Query Match   94.4%;   Score 1128.5;   DB 2;   Length 235;
Best Local Similarity   94.5%;   Pred. No. 4.1e-94;
Matches 222;   Conservative   5;   Mismatches   7;   Indels   1;   Gaps   1;

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Qy      1 MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT  60
          ||||||||||||||||||||||||||:|||||||:||:||||||||||||||||||||||
Db      1 MNHLPEHMENTLTGSQSSHASIRDIHSINPAQLMARIESYEGREKKGISDVRRTFCLIVT  60

Qy     61 FDLLFVTLLWIIELNVNGGIENTLKEKEVMQYDYYSSYFDIFPLLAVRFRKVLIIAYAVCRL 120
          |||||||:||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db     61 FDLLFVTLLWIIELNVNGGIENTLKKEVIHYDYYSSYFDIFLLAVFRFKVLLLGYAVCRL 120

Qy    121 RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA 180

Qy    181 EEENRLLIVQDASERAALIPGGLSDGQFYSPPESERAGS-EEAAEEKQDSEKPLLEL    234
          |||||||||||||||||||:|||||||||||||||||| |||||||||||||||||
Db    181 EEENRLLIVQDASERAALIPAGLSDGQFYSPPESRAGSEEEAAEEKQESEKPLLEL    235
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RESULT 6
Q6DI38_BRARE
ID   Q6DI38_BRARE   PRELIMINARY;   PRT;   227 AA.
AC Q6DI38;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE STARD3 N-terminal like.
GN Name=stard3nl;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;

Left column (RESULT 7 context):

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RG  NIH MGC Project;
RL  Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC  -----------------------------------------------------------
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----------------------------------------------------------
DR  EMBL; BC075752; AAH75752.1; -; mRNA.
DR  Ensembl; ENSDARG00000045421; Danio rerio.
DR  ZFIN; ZDB-GENE-040718-4; stard3nl.
SQ  SEQUENCE 227 AA; 25485 MW; 24C46AD8FF4985C6 CRC64;

Query Match             66.6%;  Score 796;  DB 2;  Length 227;
Best Local Similarity   68.3%;  Pred. No. 6.7e-64;
Matches  155;  Conservative  31;  Mismatches  39;  Indels  2;  Gaps  2;

Qy    8 MENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLFVT  67
          :|::|| |||||||||||||||:||| |:|||||:||||||||||||||||||||||||
Db    1 MDSQCSSSVGSRANLGSLGNINSTPISARVESYEAGEKKGISDVRRTFCLFVTFDLLFVT  60

Qy   68 LLWIIELNVNGGIENTLEKEVMQYDYSSSYFDIFLLAVFRFKVLLLAYAVCRLRHWWAIA 127
         ||||||||||||| :| |:||:|:||: ::||||| ||||||  |||||||:|||||||||
Db   61 LLWIIELNVNGGIQQQLEQEVLKYDYHKSFDIFLFLLAVFRFAAILLAYAVCKLRHWWAIA 120

Qy  128 LTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEAEEENRLL 187
         :||| | ||::| |::||::||||||| |||||||||||||| ||||||||||| :: | :|
Db  121 ITTAIITGFLIVKVVVSKLLSQGAFGYLLPIISFILAWIETWLLDFKVLPQEAGDEIRYL 180

Qy  188 IVQDASERAALI-PGGLSDGQFYSPPESEAGS--EEAEKQDSEKPLL 232
         ::|: | :  |: ||| |:| ||||||||  :|    | | |:|:|:|
Db  181 SVQNRLEHEPLLPPGPLSEGLFYSPPESLADSDEDLDDKHDLEKPIV 227
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RESULT 7
ID  Q6DFR7_XENTR    PRELIMINARY;    PRT;    448 AA.
AC  Q6DFR7;
DT  16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT  16-AUG-2004, sequence version 1.
DT  07-FEB-2006, entry version 15.
DE  Name=stard3-prov;
GN  Name=stard3-prov;
OS  Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC  Xenopodinae; Xenopus; Silurana.
OX  NCBI_TaxID=8364;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Embryo;
RX  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA  Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA  Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Embryo;
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Right column (RESULT 8 context):

```
RA  Klein S., Gerhard D.S.;
RL  Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC  -----------------------------------------------------------
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----------------------------------------------------------
DR  EMBL; BC076666; AAH76666.1; -; mRNA.
DR  SMR; Q6DFR7; 232-443.
DR  Ensembl; ENSXETG00000015141; Xenopus tropicalis.
DR  GO; GO:0015485; F:cholesterol binding; IEA.
DR  GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR  GO; GO:0006694; P:steroid biosynthesis; IEA.
DR  InterPro; IPR000799; StAR.
DR  InterPro; IPR002913; START_lipid_bd.
DR  Pfam; PF01852; START; 1.
DR  PRINTS; PR00978; STARPROTEIN.
DR  SMART; SM00234; START; 1.
DR  PROSITE; PS50848; START; 1.
SQ  SEQUENCE 448 AA; 50927 MW; 2686D07C737D4204 CRC64;

Query Match             58.6%;  Score 700.5;  DB 2;  Length 448;
Best Local Similarity   61.1%;  Pred. No. 7.3e-55;
Matches  143;  Conservative  29;  Mismatches  49;  Indels  13;  Gaps  4;

Qy    1 MNHLP-----EDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFC  56
         | :||       ||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MTKLPGDFQPDLERSLPAIASINSSMSQNHVFSPHSLLPR-----EQRRVISDVRRTFC  54

Qy   57 LFVTFDLLFVTLLLWIIELNVNGGIENTLEKEVMQYDYSSSYFDIFLLAVFRFKVLLLAYA 116
         |||||||||: ||| |||||| |:|| :| |:|:|:||: ::||||||||||| ||| ||
Db   55 LFVTFDLLFISLLMIIELNTNDGIEKNLEEEILHYDFKNSFPDIFLLAVFRFSVLLAYA 114

Qy  117 VCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVL 176
         :||||||||| :|| |||||:|||||  | | ||||||||||:||:|||||:|||||||||
Db  115 IVRLRHWWAIAITTLVTSAFLIAKVIQSGLLSKGAFGYVLPIVSFVLAWLETWFLDFKVL 174

Qy  177 PQEAEEENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSGEEAAEEKQDSEK 229
         ||||  ||   ::| : |:  ||  ||||||||||||||| |:    : :| |:|
Db  175 TQEAAEEERWYMAVQRAAGSHPPLLYNGALSDGQFYSPPESFAQSD--NEFDDDEE 226
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RESULT 8
ID  Q6PF40_XENLA    PRELIMINARY;    PRT;    444 AA.
AC  Q6PF40;
DT  05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT  05-JUL-2004, sequence version 14.
DT  07-FEB-2006, entry version 1.
DE  MGC68989 protein.
OS  Xenopus laevis (African clawed frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC  Xenopodinae; Xenopus.
OX  NCBI_TaxID=8355;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Spleen;
RX  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RESULT 9

ID   Q6GNT3_XENLA   PRELIMINARY;   PRT;   448 AA.
AC   Q6GNT3;
DT   19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   MGC80895 protein.
GN   Name=MGC80895;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.

RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
DR   EMBL; BC057738; AAH57738.1; -; mRNA.
DR   SMR; Q6PF40; 228-439.
DR   GO; GO:0015485; F:cholesterol binding; IEA.
DR   GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR   GO; GO:0006694; P:steroid biosynthesis; IEA.
DR   InterPro; IPR000799; STAR.
DR   InterPro; IPR002913; START_lipid_bd.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
SQ   SEQUENCE   444 AA;   50572 MW;   7BEA97317BF48358 CRC64;

Query Match   58.5%; Score 698.5; DB 2; Length 444;
Best Local Similarity   60.9%; Pred. No. 1.1e-54;
Matches 140; Conservative 30; Mismatches 51; Indels   9; Gaps   3;

Qy   1 MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVT 60
          :|| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MTKIPGDFQPDLERSLPAIASMSQSHVFSPRSLLPR------EQRRAISDVRRTFCLFVT 54

Qy   61 FDLLFVTLLMIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVRFKVLILAYAVCRL 120
         |||||:|||||||||||||||:|::|||:|||||||:|||||||:||||||:|:||
Db   55 FDLLFISLLMIIELNTNGIEKNLEEEILYYDFKNSFFDIFLLAVRFSVLILAVAIVRL 114

Qy 121 RHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEA 180
         |||||||:||.||||||.||:|.:|||.||||||||||:||:|||.||||||||||.||
Db 115 RHWWAIAITTLVTSAFLIVKVIQSGLLSKGAFGYVLPIVSFVLAWLETWFLDFKVLTQEA 174

Qy 181 EEENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSEEAEEKQDSEK 229
         |||.| ||||||||||| |||||||||||||||:|||| ..|| ||::
Db 175 EEERWYIAAQAAATHPSLLYNGALSDGQFYSPPESFAGSD--NEFDDEEE 222

RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073419; AAH73419.1; -; mRNA.
DR   SMR; Q6GNT3; 236-443.
DR   GO; GO:0015485; F:cholesterol binding; IEA.
DR   GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR   GO; GO:0006694; P:steroid biosynthesis; IEA.
DR   InterPro; IPR000799; STAR.
DR   InterPro; IPR002913; START_lipid_bd.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
SQ   SEQUENCE   448 AA;   51280 MW;   472FF8E7C3B2F5E4 CRC64;

Query Match   57.2%; Score 684; DB 2; Length 448;
Best Local Similarity   59.7%; Pred. No. 2.3e-53;
Matches 139; Conservative 34; Mismatches 48; Indels 12; Gaps   4;

Qy   1 MNHLP-------EDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFC 56
          :|||| ||:|||||||||||||||||||||||||||||||||||||||:||||||
Db   1 MTKLPGEFQPDLERSLPAIASINSSMSHHNVFSPHSLLPR------EQRRLLSDVRRTFC 54

Qy   57 LFVTFDLLFVTLLMIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVRFKVLILAYA 116
         ||||||||||:|||||||||||||||:|::|||:|||||||:|||||||:||||||
Db   55 LFVTFDLLFISLLMIIELNTNGIEKNLEEEILHYDFKNSFFDIFLLAVRFSVLILAYA 114

Qy 117 VCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVL 176
         :.|||||||||:||.||||||.||:|.:|||.||||||||||:||:|||.|||||||||
Db 115 IVRLRHWWAIAITTLVTSAFLIVKVIQSGLLSKGAFGYVLPIVSFVLAWLETWFLDFKVL 174

Qy 177 PQEAEEENRLLIVQ-DASERAALIPGGLSDGQFYSPPESEAGSE-EAEEKQDS 227
         .|||||| | ||||||||||||||||||||||||||:|||| .|:|:|:
Db 175 TQEAEEERWYIAAQAPANHPPYLYNGTLSDGQFYSPPESFAGSDNEFEDEEEA 227

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RESULT 10

ID   MLN64_HUMAN     STANDARD;     PRT;    445 AA.
AC   Q14849; Q96HM9;
DT   30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1996, sequence version 1.
DT   07-FEB-2006, entry version 51.
DE   MLN 64 protein (StAR-related lipid transfer protein 3) (StARD3) (START
DE   domain-containing protein 3) (CAB1 protein).
GN   Name=STARD3; Synonyms=CAB1, MLN64;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Mammary carcinoma;
RX   MEDLINE=96039245; PubMed=7490069;
RA   Tomasetto C.L., Regnier C.H., Moog-Lutz C., Mattei M.-G.,
RA   Chenard M.-P., Lidereau R., Basset P., Rio M.-C.;
RT   "Identification of four novel human genes amplified and overexpressed
RT   in breast carcinoma and localized to the q11-q21.3 region of
RT   chromosome 17.";
RL   Genomics 28:367-376(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Oesophageal carcinoma;
RX   MEDLINE=97413641; PubMed=9270027;
RA   Akiyama N., Sasaki H., Ishizuka T., Kishi T., Sakamoto H., Onda M.,
RA   Hirai H., Yazaki Y., Sugimura T., Terada M.;
RT   "Isolation of a candidate gene, CAB1, for cholesterol transport to
RT   mitochondria from the c-ERBB-2 amplicon by a modified cDNA selection
RT   method.";
RL   Cancer Res. 57:3548-3553(1997).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Lung, Skin, and Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 216-445.
RX   MEDLINE=20264523; PubMed=10802740; DOI=10.1038/75192;
RA   Tsujishita Y., Hurley J.H.;
RT   "Structure and lipid transport mechanism of a StAR-related domain.";
RL   Nat. Struct. Biol. 7:408-414(2000).
RN   [5]
RP   TOPOLOGY.
RX   MEDLINE=21264925; PubMed=11053434; DOI=10.1074/jbc.M006279200;
RA   Alpy F., Stoeckel M.-E., Dierich A., Escola J.-M., Wendling C.,
RA   Chenard M.-P., Vanier M.T., Gruenberg J., Tomasetto C., Rio M.-C.;
RT   "The steroidogenic acute regulatory protein homolog MLN64, a late
RT   endosomal cholesterol-binding protein.";
RL   J. Biol. Chem. 276:4261-4269(2001).
CC   -!- FUNCTION: Binds and transports cholesterol. Promotes
CC       steroidogenesis in placenta and brain.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC       membrane protein.
CC   -!- SIMILARITY: Contains 1 MENTAL domain.
CC   -!- SIMILARITY: Contains 1 START domain.
CC   -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC       WWW="http://www.infobiogen.fr/services/chromcancer/Genes/MLN64ID202.html"
CC
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DR   EMBL; X80198; CAA56489.1; -; mRNA.
DR   EMBL; D38255; BAA22525.1; -; mRNA.
DR   EMBL; BC008356; AAH08356.1; -; mRNA.
DR   EMBL; BC009747; AAH08747.1; -; mRNA.
DR   EMBL; BC025679; AAH25679.1; -; mRNA.
DR   PIR; I38027; I38027.
DR   PDB; 1EM2; X-ray; A=216-444.
DR   Ensembl; ENSG00000131748; Homo sapiens.
DR   H-InvDB; HIX0013780; -.
DR   HGNC; HGNC:17579; STARD3.
DR   MIM; 607048; gene.
DR   GO; GO:0005737; C:cytoplasm; TAS.
DR   GO; GO:0008203; P:cholesterol metabolism; TAS.
DR   GO; GO:0006629; P:lipid metabolism; TAS.
DR   GO; GO:0006839; P:mitochondrial transport; TAS.
DR   GO; GO:0008202; P:steroid metabolism; TAS.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START_lipid_bd.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
KW   3D-structure; Lipid transport; Lipid-binding; Membrane;
KW   Steroidogenesis; Transmembrane; Transport.
FT   CHAIN         1    445       MLN 64 protein.
FT                                /FTId=PRO_0000220653.
FT   TOPO_DOM      1     51       Cytoplasmic (Potential).
FT   TRANSMEM     52     72       Potential.
FT   TOPO_DOM     73     94       Extracellular (Potential).
FT   TRANSMEM     95    115       Potential.
FT   TOPO_DOM    116    120       Cytoplasmic (Potential).
FT   TRANSMEM    121    141       Potential.
FT   TOPO_DOM    142    148       Extracellular (Potential).
FT   TRANSMEM    149    169       Potential.
FT   TOPO_DOM    170    445       Cytoplasmic (Potential).
FT   DOMAIN       46    217       MENTAL.
FT   DOMAIN      230    443       START.
FT   CONFLICT    117    117       Q -> R (in Ref. 3; AAH25679).
FT   CONFLICT    216    216       G -> R (in Ref. 3; AAH25679).
FT   HELIX       233    258
FT   STRAND      260    264
FT   STRAND      266    267
FT   TURN        270    276
FT   STRAND      277    279
FT   TURN        280    291
FT   HELIX       293    299
FT   TURN        300    302
FT   HELIX       304    307
FT   HELIX       308    310
FT   TURN        312    313
FT   TURN        314    323
FT   STRAND      324    326
FT   STRAND      327    334
FT   TURN        337    337
FT   STRAND      338    341
FT   STRAND      342    342
FT   TURN        345    355
FT   STRAND      357    366
FT   TURN        370    371
FT   TURN        370    372
FT   STRAND      372    372
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FT   TURN        376    377
FT   STRAND      378    380
FT   STRAND      382    383
FT   STRAND      385    392
FT   STRAND      394    395
FT   TURN        397    398
FT   STRAND      400    406
FT   STRAND      408    409
FT   STRAND      412    414
FT   HELIX       416    440
FT   TURN        441    442
SQ   SEQUENCE    445 AA;  50474 MW;  62BED5C3EDA0DDEF CRC64;

RESULT 11
ID   Q53Y53_HUMAN            PRELIMINARY;      PRT;     445 AA.
AC   Q53Y53;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   START domain containing 3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT   vector.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; BT006964; AAP35610.1; -; mRNA.
DR   SMR; Q53Y53; 230-443.
DR   Ensembl; ENSG00000131748; Homo sapiens.
DR   GO; GO:0015485; F:cholesterol binding; IEA.
DR   GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR   GO; GO:0006694; P:steroid biosynthesis; IEA.
DR   InterPro; IPR000799; START.
DR   InterPro; IPR002913; START_lipid_bd.
DR   Pfam; PF01852; START; 1.
DR   PRINTS; PR00078; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
SQ   SEQUENCE    445 AA;  50474 MW;  62BED5C3EDA0DDEF CRC64;

Query Match             55.6%;  Score 664;  DB 1;  Length 445;
Best Local Similarity   56.2%;  Pred. No. 1.5e-51;
Matches  135;  Conservative  38;  Mismatches  45;  Indels  22;  Gaps  5;

Qy          1 MNHLP-------EDMENAL------TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDV 51
              |: | ||          |:  | |::  || | | ||||:: |
Db          1 MSKLPRELTRDLERSLPAVASLGSSLSHSQSLSSHLLPPE-----------KRRAISDV 49

Qy         52 RRTFCLFVTFDLLFVTLLMIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVRFKVL 111
              :|||||||||||||:||||||||||||||:||:||: || ||||||:|:::|||||||
Db         50 RRTFCLFVTFDLLFISLLMWIIELNTNTGIRKNLEQEIIQYNFKTSFFDIFVLAFFRSGL 109

Qy        112 ILAYAVCRLRHWNAIALTTRAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFL 171
              |||||||||||||:|||||||||||||||||||||||||||||||||||::||||||||||
Db        110 LLGYAVLQLRHWWVIAVTTLVSSAFLIVKVILSELLSKGAFGYLLPIVSFVLAWLETWFL 169

Qy        172 DFKVLPQEAEEENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSE-EAAEKQDSEK 229
              |||||||||||||||||||||||||||| |||||||||||| ||||||| |:|||||||
Db        170 DFKVLPQEAEEERWYLAAQVAVARGPLLFSGALSEGQFYSPPESPFAGSDNESDEEVAGKK 229

RESULT 12
ID   MLN64_MOUSE             STANDARD;      PRT;     446 AA.
AC   Q61542;
DT   30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1996, sequence version 1.
DT   07-FEB-2006, entry version 45.
DE   MLN 64 protein (StAR-related lipid transfer protein 3) (StARD3) (START
DE   domain-containing protein 3) (ES 64 protein).
GN   Name=Stard3; Synonyms=Es64, Mln64;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=96039245; PubMed=7490069;
RA   Tomasetto C.L., Regnier C.H., Moog-Lutz C., Mattei M.-G.,
RA   Chenard M.-P., Lidereau R., Basset P., Rio M.-C.;
RT   "Identification of four novel human genes amplified and overexpressed
RT   in breast carcinoma and localized to the q11-q21.3 region of
RT   chromosome 17.";
RL   Genomics 28:367-376(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Binds and transports cholesterol. Promotes
CC       steroidogenesis in placenta and brain (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
CC       membrane protein (By similarity).
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Query Match   55.6%; Score 664; DB 2; Length 445;
Best Local Similarity   56.2%; Pred. No. 1.5e-51;
Matches 135; Conservative 38; Mismatches 45; Indels 22; Gaps 5;

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Qy          1 MNHLP-------EDMENAL------TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDV 51
              |: | ||          |:  | |::  || | | ||||:: |
Db          1 MSKLPRELTRDLERSLPAVASLGSSLSHSQSLSSHLLPPE-----------KRRAISDV 49

Qy         52 RRTFCLFVTFDLLFVTLLMIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVRFKVL 111
              :|||||||||||||:||||||||||||||:||:||: || ||||||:|:::|||||||
Db         50 RRTFCLFVTFDLLFISLLMWIIELNTNTGIRKNLEQEIIQYNFKTSFFDIFVLAFFRSGL 109

Qy        112 ILAYAVCRLRHWNAIALTTRAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFL 171
              |||||||||||||:|||||||||||||||||||||||||||||||||||::||||||||||
Db        110 LLGYAVLQLRHWWVIAVTTLVSSAFLIVKVILSELLSKGAFGYLLPIVSFVLAWLETWFL 169

Qy        172 DFKVLPQEAEEENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSE-EAAEKQDSEK 229
              |||||||||||||||||||||||||||| |||||||||||| ||||||| |:|||||||
Db        170 DFKVLPQEAEEERWYLAAQVAVARGPLLFSGALSEGQFYSPPESPFAGSDNESDEEVAGKK 229
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CC   -!- SIMILARITY: Contains 1 MENTAL domain.
CC   -!- SIMILARITY: Contains 1 START domain.
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; X82457; CAA57834.1; -; mRNA.
DR   EMBL; BC003313; AAH03313.1; -; mRNA.
DR   HSSP; Q14849; 1EM2.
DR   SMR; Q61542; 231-444.
DR   Ensembl; ENSMUSG00000018167; Mus musculus.
DR   MGI; MGI:1929618; Stard3.
GO   GO; GO:0016021; C:integral to membrane; TAS.
GO   GO; GO:0005770; C:late endosome; TAS.
DR   InterPro; IPR000799; StAR.
DR   InterPro; IPR002913; START.
DR   Pfam; PF01852; START; 1.
DR   Pfam; PF01852; START_lipid_bd.
DR   PRINTS; PR00978; STARPROTEIN.
DR   SMART; SM00234; START; 1.
DR   PROSITE; PS50848; START; 1.
KW   Lipid transport; Lipid-binding; Membrane; Steroidogenesis;
KW   Transmembrane; Transport.
FT   CHAIN         1    446       MLN 64 protein.
FT                                /FTId=PRO_0000220654.
FT   TOPO_DOM      1     52       Cytoplasmic (Potential).
FT   TRANSMEM     53     73       Potential.
FT   TOPO_DOM     74     95       Extracellular (Potential).
FT   TRANSMEM     96    116       Potential.
FT   TOPO_DOM    117    121       Cytoplasmic (Potential).
FT   TRANSMEM    122    142       Potential.
FT   TOPO_DOM    143    149       Extracellular (Potential).
FT   TRANSMEM    150    170       Potential.
FT   TOPO_DOM    171    446       Cytoplasmic (Potential).
FT   DOMAIN       47    218       MENTAL.
FT   DOMAIN      231    444       START.
SQ   SEQUENCE   446 AA;  50470 MW;  DBF435960AF3E1E2 CRC64;

RESULT 13
Q54C3_MOUSE
ID   Q54C3_MOUSE     PRELIMINARY;     PRT;    446 AA.
AC   Q54C3;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   3 days neonate thymus cDNA, RIKEN full-length enriched library,
DE   clone:A630020B16 product:steroidogenic acute regulatory protein
DE   related full insert sequence (NOD-derived library, clone:F630202P06
DE   product:START domain containing 3, full insert sequence).
GN   Name=Stard3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Query Match             54.9%;
Best Local Similarity   57.8%;
Matches  133;  Conservative  33;  Mismatches  47;  Indels  17;  Gaps  4;

Score 656.5;  DB 1;  Length 446;
Pred. No. 7.3e-51;

Qy    7  DMENAL------TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTF  61
            |:|||              .:.:               :::||||||||||||||
Db   11  DLERSLPALASLGTSLSHGQSLSSHFIPPL---------EKRRAISDVRRTFCLFVTF  60

Qy   62  DLLFVTLIWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLLIAYAVCRLR  121
            |||:.|:|||||||:.|.||:.:||:|.|:|:.||:|||||:|.||||:.|||.:|.|:
Db   61  DLLFISLLWIIELNTNTGIRKNLEQEVIHYSFQSSFFDIFVLAFFRFSGLLIGYAVLRLQ  120

Qy  122  HWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPQEAE  181
            |||.|.:|.|.:||||:.||||:.|:|.||||||:||::||:|||:|||||||||||||||
Db  121  HWWVIAVTLVSSAFLIVKVILSELLSKGAFGYLLPIVSFVLAWLETWFLDFKVLPQEAE  180

Qy  182  EENRLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSE-EAEEKQDSEK  229
            ||..:.|.:.|..:..|| .||||..|||||||||.|||.:||:||..:.|
Db  181  EERWYIAAQAAVARGPLIFSGALSSGQFYSPPESFAGSDNESDEEVTGKK  230
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OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090.
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Thymus;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Thymus;
RG   RIKEN Genome Exploration Research Group and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Thymus;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
```

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi L., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C.A., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [8]

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi T., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN [9]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AK041538; BAC30977.1; -; mRNA.
DR EMBL; AK155124; BAE33063.1; -; mRNA.
DR SMR; Q5U2T5; 231-444.
DR Ensembl; ENSMUSG00000018167; Mus musculus.
DR MGI; MGI:1929618; Stard3.
DR GO; GO:0016021; C:integral to membrane; RCA.
DR GO; GO:0005770; C:late endosome; TAS.
DR GO; GO:0005770; C:late endosome; TAS.
DR InterPro; IPR000799; StAR.
DR InterPro; IPR002913; START_lipid_bd.
DR Pfam; PF01852; START; 1.
DR PRINTS; PR00978; STARPROTEIN.
DR SMART; SM00234; START; 1.
DR PROSITE; PS50848; START; 1.
SQ SEQUENCE 446 AA; 50470 MW; DBF435960 4F3E1E2 CRC64;

Qy   7 DMENAL------TGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTF 61
           |:|:|| :|||::| :| :| :| |:|| :||| : |||||||||||||
Db   11 DLERSLPALASLGISLSHSQSLSSHFIPPL------EKRRAISDVRRTFCLFVTF 60

Qy   62 DLLFVTLIWIIELNVNGGIENTLLEKEVMQYDYSYSYFDIFLLAVRFKVLILLAYAVCRLR 121
           ||||:.|:|||||| |:||| :| :||:::| .|::|||||:||::| ||| |||| ||:
Db   61 DLLFISLLWIIELNTNTGIRKNLEQEVIHYSFQSSFFDIFVLAFPRFSGLLLGYAVLRLQ 120

Qy   122 HWWAIALTTRAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILLAWIETWFLDFKVLPQEAE 181
           |||.||: : ..||:||:.|||||:| :|||||:|||:.||:|||:|||| |||||||||
Db   121 HWWVIAVTLVSSAFLIVKVILSELLSKGAFGYLLPIVSFVLAWLETWFDLDFKVLPQEAE 180

Qy   182 EENRLLIVQDASERAALI-PGGLSDGQFYSPPESSEAGSE-EAEEKQDSEK 229
           ||. |: : |... .| .|.||:|||||||||| .||: :||:: ..|:
Db   181 EERWYLAAQAAVARGPLLFSGALSEGQFYSPPESFAGSDNESDEEVTGKK 230

Query Match   54.9%; Score 656.5; DB 2; Length 446;
Best Local Similarity   57.8%; Pred. No.   7.3e-51;
Matches 133; Conservative 33; Mismatches 47; Indels 17; Gaps 4;

RESULT 14
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ID   Q5U2T5_RAT   PRELIMINARY;   PRT;   446 AA.
AC   Q5U2T5;
DT   07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT   07-DEC-2004, sequence version 1.
DT   07-FEB-2006, entry version 14.
DE   Hypothetical LOC363675.
GN   Name=LOC363675;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.

Left column

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OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Heart;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Heart;
RG   NIH MGC Project;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
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DR   EMBL; BC085872; AAH85872.1; -; mRNA.
SMR; Q5U2T5; 231-444.
GO; GO:0015485; F:cholesterol binding; IEA.
GO; GO:0017127; F:cholesterol transporter activity; IEA.
GO; GO:0006694; P:steroid biosynthesis; IEA.
InterPro; IPR000799; StAR.
Pfam; PF01852; START; 1.
InterPro; IPR002913; START_lipid_bd.
PRINTS; PR00978; STARPROTEIN.
SMART; SM00234; START; 1.
PROSITE; PS50848; START; 1.
Hypothetical protein.
SQ   SEQUENCE   446 AA;  50386 MW;  19BF58B56F09722F CRC64;
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Query Match             54.9%;  Score 656.5;  DB 2;  Length 446;
Best Local Similarity   56.2%;  Pred. No. 7.3e-51;
Matches  135;  Conservative  32;  Mismatches  52;  Indels  21;  Gaps  4;

Qy       1  MNHLPEDMEN------------ALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDV  51
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Db       1  MSKLPGDLAGDLERSLPALASLGTSLSHSQSLSSHFIPPPLEKRRV----------VSDV  50

Qy      52  RRTFCLFVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVL  111
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Db      51  RRTFCLFVTFDLLFISLLWIELNTNGIRKNLEQEVIHYSFQSSFFDIFVLAAFRFRFSGL  110

Qy     112  IIAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFL  171
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Db     111  LIGYAVLRLQHWWVIAITLVSSAFLIVKVIISELLSKGAFGYLLPIVSFVLAWLETWFL  170

Qy     172  DFKVLPQEAEEENRLLIVQDASERAALI-PGGLSDGQFYSPPESPESEAGSE-EAEEKQDSEK  229
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Db     171  DFKVLPQEAEERWYLAAQAAVARGPLLFSGALSEQQFYSPPESFAGSDSESDEEVAGKK  230
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Right column

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DT   06-JUN-2002, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-2005, sequence version 2.
DT   07-FEB-2006, entry version 21.
DE   MLN64-like protein (START domain-containing protein 3).
GN   Name=stard3; Synonyms=mln64;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=AB;
RG   NIH - Zebrafish Gene Collection (ZGC) project;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 210-448.
RX   PubMed=11064158; DOI=10.1016/S0303-7207(00)00316-6;
RA   Bauer M.P., Bridgham J.T., Langenau D.M., Johnson A.L., Goetz F.W.;
RT   "Conservation of steroidogenic acute regulatory (StAR) protein
RT   structure and expression in vertebrates.";
RL   Mol. Cell. Endocrinol. 168:119-125(2000).
CC   -!- FUNCTION: Binds and transports cholesterol. Promotes
CC       steroidogenesis (By similarity).
CC   -!- SIMILARITY: Contains 1 START domain.
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DR   EMBL; BC056766; AAH56766.1; -; mRNA.
DR   EMBL; AF258786; AAG28603.1; -; mRNA.
HSSP; Q14849; 1EM2.
SMR; Q9DFS4; 232-443.
Ensembl; ENSDARG00000017809; Danio rerio.
ZFIN; ZDB-GENE-001120-2; stard3.
InterPro; IPR000799; StAR.
InterPro; IPR002913; START_lipid_bd.
Pfam; PF01852; START; 1.
PRINTS; PR00978; STARPROTEIN.
SMART; SM00234; START; 1.
PROSITE; PS50848; START; 1.
KW   Lipid transport; Lipid-binding; Steroidogenesis; Transport.
FT   DOMAIN      232    445    START.
FT   CONFLICT    210    220    Missing (in Ref. 2).
FT                            /FTId=PRO_0000220655.
FT   CHAIN         1    448    MLN64-like protein.
FT                            /FTId=PRO_0000220655.
SQ   SEQUENCE   448 AA;  50751 MW;  716A18C127B59C5D CRC64;
PGRPRVRPRVR
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Best Local Similarity   70.9%;  Pred. No. 1.2e-48;
Matches  127;  Conservative  18;  Mismatches  32;  Indels  2;  Gaps  2;

Qy      44  EKRGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLL  103
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Db      43  ERKAFSDVRRTFCLFVTFDLLFITLLWIELNISKSIWNSLENEVHVNFKSSFFDIFLL  102

Qy     104  AVFRFKVLILAYAVCRLRHWWAIALTTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFTL  163
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Db     103  AVFRFLCLQLGYAAFRLRHWWIAITLVTTAFLIAKVILSDLFSQNAFGYVLPITSFVV  162

Qy     164  AWIETWFLDFKVLPQERAEEEN-RLLIVQDASERAALI-PGGLSDGQFYSPPESEAGSEE  220
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Db     163  AWLETWFLDFKVLTQERAEDERYYLAAVNAACPAPLLCPRPVSDGQFYSPPESLAGSED  221
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Far-left RESULT block

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RESULT 15
MLN64_BRARE
ID   MLN64_BRARE             STANDARD;      PRT;   448 AA.
AC   Q9DFS4; Q6PH03;
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